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(54) **L-AMINO ACID-PRODUCING BACTERIA AND PROCESS FOR PRODUCING L-AMINO ACID**

(57) An L-amino acid is produced by culturing a *Methylophilus* bacterium which can grow by using methanol as a main carbon source and has L-amino acid-producing ability, for example, a *Methylophilus* bacterium in which dihydrodipicolinate synthase activity and aspartokinase activity are enhanced by transformation through introduction into cells, of a DNA coding for dihydrodipicolinate synthase that does not suffer feed-

back inhibition by L-lysine and a DNA coding for aspartokinase that does not suffer feedback inhibition by L-lysine, or a *Methylophilus* bacterium made to be casamino acid auxotrophic, in a medium containing methanol as a main carbon source, to produce and accumulate an L-amino acid in culture, and collecting the L-amino acid from the culture.

EP 1 188 822 A1

Description

TECHNICAL FIELD

5 [0001] The present invention relates to techniques in the field of microbial industry. In particular, the present invention relates to a method for producing an L-amino acid by fermentation, and a microorganism used in the method.

BACKGROUND ART

10 [0002] Amino acids such as L-lysine, L-glutamic acid, L-threonine, L-leucine, L-isoleucine, L-valine and L-phenylalanine are industrially produced by fermentation by using microorganisms that belong to the genus *Brevibacterium*, *Corynebacterium*, *Bacillus*, *Escherichia*, *Streptomyces*, *Pseudomonas*, *Arthrobacter*, *Serratia*, *Penicillium*, *Candida* or the like. In order to improve the productivity, strains isolated from nature or artificial mutants thereof have been used as these microorganisms. Various techniques have been disclosed for enhancing activities of L-glutamic acid biosynthetic enzymes by using recombinant DNA techniques, to increase the L-glutamic acid-producing ability.

15 [0003] The productivity of L-amino acids has been considerably increased by breeding of microorganisms such as those mentioned above and the improvement of production methods. However, in order to meet further increase in the demand in future, development of methods for more efficiently producing L-amino acids at lower cost have still been desired.

20 [0004] As methods for producing amino acids by fermentation of methanol which is a fermentation raw material available in a large amount at a low cost, there have conventionally known methods using microorganisms that belong to the genus *Achromobacter* or *Pseudomonas* (Japanese Patent Publication (Kokoku) No. 45-25273/1970), *Protaminobacter* (Japanese Patent Application Laid-open (Kokai) No. 49-125590/1974), *Protaminobacter* or *Methanomonas* (Japanese Patent Application Laid-open (Kokai) No. 50-25790/1975), *Microcycilus* (Japanese Patent Application Laid-open (Kokai) No. 52-18886/1977), *Methylobacillus* (Japanese Patent Application Laid-open (Kokai) No. 4-91793/1992), *Bacillus* (Japanese Patent Application Laid-open (Kokai) No. 3-505284/1991) and so forth.

25 [0005] So far, however, no method has been known for producing L-amino acids by using *Methylophilus* bacteria. Although methods described in EP 0 035 831 A, EP 0 037 273 A and EP 0 066 994 A have been known as methods for transforming *Methylophilus* bacteria by using recombinant DNA, applying recombinant DNA techniques to improvement of amino acid productivity of *Methylophilus* bacteria has not been known.

DISCLOSURE OF THE INVENTION

35 [0006] The object of the present invention is to provide a novel L-amino acid-producing bacterium and a method for producing an L-amino acid by using the L-amino acid-producing bacterium.

[0007] As a result of the present inventors' efforts devoted to achieve the aforementioned object, they found that *Methylophilus* bacteria were suitable for producing L-amino acids. Further, although it has conventionally been considered difficult to obtain auxotrophic mutants of *Methylophilus* bacteria (FEMS Microbiology Rev. 39, 235-258 (1986) and Antonie van Leeuwenhoek 53, 47-53 (1987)), the present inventors have succeeded in obtaining auxotrophic mutants of said bacteria. Thus, the present invention has been accomplished.

40 [0008] That is, the present invention provides the followings.

- (1) A *Methylophilus* bacterium having L-amino acid-producing ability.
- 45 (2) The *Methylophilus* bacterium according to (1), wherein the L-amino acid is L-lysine, L-valine, L-leucine, L-isoleucine or L-threonine.
- (3) The *Methylophilus* bacterium according to (1), which has resistance to an L-amino acid analogue or L-amino acid auxotrophy.
- (4) The *Methylophilus* bacterium according to (1), wherein L-amino acid biosynthetic enzyme activity is enhanced.
- 50 (5) The *Methylophilus* bacterium according to (1), wherein dihydrodipicolinate synthase activity and aspartokinase activity are enhanced, and the bacterium has L-lysine-producing ability.
- (6) The *Methylophilus* bacterium according to (1), wherein dihydrodipicolinate synthase activity is enhanced, and the bacterium has L-lysine-producing ability.
- (7) The *Methylophilus* bacterium according to (1), wherein aspartokinase activity is enhanced, and the bacterium has L-lysine-producing ability.
- 55 (8) The *Methylophilus* bacterium according to any one of (5) to (7), wherein an activity or activities of one, two or three of enzymes selected from aspartic acid semialdehyde dehydrogenase, dihydrodipicolinate reductase and diaminopimelate decarboxylase is/are enhanced.
- (9) The *Methylophilus* bacterium according to (5), wherein the dihydrodipicolinate synthase activity and the aspar-

tokenase activity are enhanced by transformation through introduction into cells, of a DNA coding for dihydrodipicolinate synthase that does not suffer feedback inhibition by L-lysine and a DNA coding for aspartokinase that does not suffer feedback inhibition by L-lysine.

5 (10) The bacterium according to (1), wherein activities of aspartokinase, homoserine dehydrogenase, homoserine kinase and threonine synthase, and the bacterium has L-threonine-producing ability.

(11) The bacterium according to any one of (1) to (10), wherein the *Methylophilus* bacterium is *Methylophilus methylotrophus*.

10 (12) A method for producing an L-amino acid, which comprises culturing a *Methylophilus* bacterium as defined in any one of the above (1) to (11) in a medium to produce and accumulate an L-amino acid in culture and collecting the L-amino acid from the culture.

(13) The method according to (12), wherein the medium contains methanol as a main carbon source.

(14) A method for producing bacterial cells of a *Methylophilus* bacterium with an increased content of an L-amino acid, which comprises culturing a *Methylophilus* bacterium as defined in any one of the above (1) to (11) in a medium to produce and accumulate an L-amino acid in bacterial cells of the bacterium.

15 (15) The method for producing bacterial cells of the *Methylophilus* bacterium according to (14), wherein the L-amino acid is L-lysine, L-valine, L-leucine, L-isoleucine or L-threonine.

(16) A DNA which codes for a protein defined in the following (A) or (B):

20 (A) a protein which has the amino acid sequence of SEQ ID NO: 6, or

(B) a protein which has an amino acid sequences of SEQ ID NO: 6 including substitution, deletion, insertion, addition or inversion of one or several amino acids, and has aspartokinase activity.

(17) The DNA according to (16), which is a DNA defined in the following (a) or (b):

25 (a) a DNA which has a nucleotide sequence comprising the nucleotide sequence of the nucleotide numbers 510 to 1736 of SEQ ID NO: 5; or

(b) a DNA which is hybridizable with a probe having the nucleotide sequence of the nucleotide numbers 510 to 1736 of SEQ ID NO: 5 or a part thereof under a stringent condition, and codes for a protein having aspartokinase activity.

30

(18) A DNA which codes for a protein defined in the following (C) or (D):

(C) a protein which has the amino acid sequence of SEQ ID NO: 8, or

35 (D) a protein which has an amino acid sequences of SEQ ID NO: 8 including substitution, deletion, insertion, addition or inversion of one or several amino acids, and has aspartic acid semialdehyde dehydrogenase activity.

(19) The DNA according to (18), which is a DNA defined in the following (c) or (d):

40 (c) a DNA which has a nucleotide sequence comprising the nucleotide sequence of the nucleotide numbers 98 to 1207 of SEQ ID NO: 7; or

(d) a DNA which is hybridizable with a probe having the nucleotide sequence of the nucleotide numbers 98 to 1207 of SEQ ID NO: 7 or a part thereof under a stringent condition, and codes for a protein having aspartic acid semialdehyde dehydrogenase activity.

45

(20) A DNA which codes for a protein defined in the following (E) or (F):

(E) a protein which has the amino acid sequence of SEQ ID NO: 10, or

50 (F) a protein which has an amino acid sequences of SEQ ID NO: 10 including substitution, deletion, insertion, addition or inversion of one or several amino acids, and has dihydrodipicolinate synthase activity.

(21) The DNA according to (20), which is a DNA defined in the following (e) or (f):

55 (e) a DNA which has a nucleotide sequence comprising the nucleotide sequence of the nucleotide numbers 1268 to 2155 of SEQ ID NO: 9; or

(f) a DNA which is hybridizable with a probe having the nucleotide sequence of the nucleotide numbers 1268 to 2155 of SEQ ID NO: 9 or a part thereof under a stringent condition, and codes for a protein having dihydrodipicolinate synthase activity.

(22) A DNA which codes for a protein defined in the following (G) or (H):

(G) a protein which has the amino acid sequence of SEQ ID NO: 12, or

(H) a protein which has an amino acid sequences of SEQ ID NO: 12 including substitution, deletion, insertion, addition or inversion of one or several amino acids, and has dihydrodipicolinate reductase activity.

(23) The DNA according to (22), which is a DNA defined in the following (g) or (h):

(g) a DNA which has a nucleotide sequence comprising the nucleotide sequence of the nucleotide numbers 2080 to 2883 of SEQ ID NO: 11; or

(h) a DNA which is hybridizable with a probe having the nucleotide sequence of the nucleotide numbers 2080 to 2883 of SEQ ID NO: 11 or a part thereof under a stringent condition, and codes for a protein having dihydrodipicolinate reductase activity.

(24) A DNA which codes for a protein defined in the following (I) or (J):

(I) a protein which has the amino acid sequence of SEQ ID NO: 14, or

(J) a protein which has an amino acid sequences of SEQ ID NO: 14 including substitution, deletion, insertion, addition or inversion of one or several amino acids, and has diaminopimelate decarboxylase activity.

(25) The DNA according to (24), which is a DNA defined in the following (i) or (j):

(i) a DNA which has a nucleotide sequence comprising the nucleotide sequence of the nucleotide numbers 751 to 1995 of SEQ ID NO: 13; or

(j) a DNA which is hybridizable with a probe having the nucleotide sequence of the nucleotide numbers 751 to 1995 of SEQ ID NO: 13 or a part thereof under a stringent condition, and codes for a protein having diaminopimelate decarboxylase activity.

[0009] In the present specification, "L-amino acid-producing ability" refers to ability to accumulate a significant amount of an L-amino acid in a medium or to increase the amino acid content in the microbial cells when a microorganism of the present invention is cultured in the medium.

BRIEF DESCRIPTION OF THE DRAWINGS

[0010]

Fig. 1 shows the production process of plasmid RSF24P having a mutant *dapA*. The "*dapA**24" refers to a mutant *dapA* that codes for a mutant DDPS wherein the 118-histidine residue is replaced with a tyrosine residue.

Fig. 2 shows the production process of plasmid RSFD80 having a mutant *dapA* and a mutant *lysC*. The "*lysC**80" refers to a mutant *lysC* that codes for a mutant AKIII wherein the 352-threonine residue is replaced with an isoleucine residue.

Fig. 3 shows aspartokinase activity of transformant *E. coli* strains containing an *ask* gene.

Fig. 4 shows aspartic acid semialdehyde dehydrogenase activity of transformant *E. coli* strains containing an *asd* gene.

Fig. 5 shows dihydrodipicolinate synthase activity of transformant *E. coli* strains containing a *dapA* gene.

Fig. 6 shows dihydrodipicolinate reductase activity of a transformant *E. coli* strain containing a *dapB* gene.

Fig. 7 shows diaminopimelate decarboxylase activity of transformant *E. coli* strains containing a *lysA* gene.

BEST MODE FOR CARRYING OUT THE INVENTION

<1> Microorganism of the present invention

[0011] The microorganism of the present invention is a bacterium belonging to the genus *Methylophilus* and having L-amino acid-producing ability. The *Methylophilus* bacterium of the present invention includes, for example, *Methylophilus methylotrophus* AS1 strain (NCIMB10515) and so forth. The *Methylophilus methylotrophus* AS1 strain (NCIMB10515) is available from National Collections of Industrial and Marine Bacteria (Address: NCIMB Ltd., Torry Research Station 135, Abbey Road, Aberdeen AB9 8DG, United Kingdom).

[0012] L-Amino acids produced according to the present invention include L-lysine, L-glutamic acid, L-threonine, L-

valine, L-leucine, L-isoleucine, L-tryptophan, L-phenylalanine, L-tyrosine and so forth. One or more types of such amino acids may be produced.

[0013] *Methylophilus* bacteria having L-amino acid-producing ability can be obtained by imparting L-amino acid-producing ability to wild strains of *Methylophilus* bacteria. In order to impart L-amino acid-producing ability, there can be used methods conventionally adopted for breeding coryneform bacteria, *Escherichia* bacteria or the like, such as those methods for obtaining auxotrophic mutant strains, strains resistant to L-amino acid analogues or metabolic control mutant strains, and methods for producing recombinant strains wherein L-amino acid biosynthetic enzyme activities are enhanced (see "Amino Acid Fermentation", the Japan Scientific Societies Press [Gakkai Shuppan Center], 1st Edition, published on May 30, 1986, pp.77 to 100). In breeding of amino acid-producing bacteria, the characteristic such as auxotrophy, L-amino acid analogue resistance and metabolic control mutation may be imparted alone or in combination of two or more. The L-amino acid biosynthetic enzyme activity may be enhanced alone or in combination of two or more. Further, imparting of the characteristic such as auxotrophy, L-amino acid analogue resistance and metabolic control mutation may be combined with enhancement of the L-amino acid biosynthesis enzyme activity.

[0014] For example, L-lysine-producing bacteria are bred as mutants exhibiting auxotrophy for L-homoserine or L-threonine and L-methionine (Japanese Patent Publication. (Kokoku) Nos. 48-28078/1973 and 56-6499/1981), mutants exhibiting auxotrophy for inositol or acetic acid (Japanese Patent Application Laid-open (Kokai) Nos. 55-9784/1980 and 56-8692/1981), or mutants that are resistant to oxalysine, lysine hydroxamate, S-(2-aminoethyl)-cysteine, γ -methyllysine, α -chlorocaprolactam, DL- α -amino- ϵ -caprolactam, α -aminolauryllactam, aspartic acid analogue, sulfa drug, quinoid or N-lauroylleucine.

[0015] Further, L-glutamic acid-producing bacteria can be bred as mutants exhibiting auxotrophy for oleic acid or the like. L-Threonine-producing bacteria can be bred as mutants resistant to α -amino- β -hydroxyvaleric acid. L-Homoserine-producing bacteria can be bred as mutants exhibiting auxotrophy for L-threonine or mutants resistant to L-phenylalanine analogues. L-Phenylalanine-producing bacteria can be bred as mutants exhibiting auxotrophy for L-tyrosine. L-Isoleucine-producing bacteria can be bred as mutants exhibiting auxotrophy for L-leucine. L-Proline-producing bacteria can be bred as mutants exhibiting auxotrophy for L-isoleucine.

[0016] Furthermore, as mentioned in the examples hereinafter, strains that produce one or more kinds of branched amino acids (L-valine, L-leucine and L-isoleucine) can be obtained as strains exhibiting auxotrophy for casamino acid.

[0017] In order to obtain mutants from *Methylophilus* bacteria, the inventors of the present invention first examined details of an optimal mutagenesis condition by using emergence frequency of streptomycin resistant strains as an index. As a result, the maximum emergence frequency of streptomycin resistant strains was obtained when the survival rate after mutagenesis was about 0.5%, and they succeeded in obtaining auxotrophic strains under this condition. They also succeeded in obtaining auxotrophic strains, which had been considered difficult, by largely scaling up the screening of mutants compared with that previously conducted for *E. coli* and so forth.

[0018] As described above, since it has been revealed that mutants can be obtained by mutagenizing *Methylophilus* bacteria under a suitable condition, it has become possible to readily obtain desired mutants by suitably setting such a condition that the survival rate after the mutagenesis should become about 0.5%, depending on the mutagenesis method.

[0019] Mutagenesis methods for obtaining mutants from *Methylophilus* bacteria include UV irradiation and treatments with mutagenesis agents used for usual mutagenesis treatments such as N-methyl-N'-nitro-N-nitrosoguanidine (NTG) and nitrous acid. *Methylophilus* bacteria having L-amino acid-producing ability can also be obtained by selecting naturally occurring mutants of *Methylophilus* bacteria.

[0020] L-Amino acid analogue-resistant mutants can be obtained by, for example, inoculating mutagenized *Methylophilus* bacteria to an agar medium containing an L-amino acid analogue at a variety of concentrations and selecting strains that form colonies.

[0021] Auxotrophic mutants can be obtained by allowing *Methylophilus* bacteria to form colonies on an agar medium containing a target nutrient (for example, L-amino acid), replicating the colonies to an agar medium not containing said nutrient, and selecting strains that cannot grow on the agar medium not containing the nutrient.

[0022] Methods for imparting or enhancing L-amino acid-producing ability by enhancing L-amino acid biosynthetic enzyme activity will be exemplified below.

[L-Lysine]

[0023] L-Lysine-producing ability can be imparted by, for example, enhancing dihydrodipicolinate synthase activity and/or aspartokinase activity.

[0024] The dihydrodipicolinate synthase activity and/or the aspartokinase activity in *Methylophilus* bacteria can be enhanced by ligating a gene fragment coding for dihydrodipicolinate synthase and/or a gene fragment coding for aspartokinase with a vector that functions in *Methylophilus* bacteria, preferably a multiple copy type vector, to create a recombinant DNA, and introducing them into a *Methylophilus* bacterium host to transform the host. As a result of the

increase in the copy numbers of the gene coding for dihydrodipicolinate synthase and/or the gene coding for aspartokinase in cells of the transformant strain, the activity or activities thereof is/are enhanced. Hereafter, dihydrodipicolinate synthase, aspartokinase and aspartokinase III are also referred with abbreviations of DDPS, AK and AKIII, respectively.

5 [0025] As a microorganism providing a gene that codes for DDPS and a gene that codes for AK, any microorganisms can be used so long as they have genes enabling expression of DDPS activity and AK activity in microorganisms belonging to the genus *Methylophilus*. Such microorganisms may be wild strains or mutant strains derived therefrom. Specifically, examples of such microorganisms include *E. coli* (*Escherichia coli*) K-12 strain, *Methylophilus methylotrophus* AS1 strain (NCIMB10515) and so forth. Since nucleotide sequences of a gene coding for DDPS (*dapA*, Rich-

10 aud, F. et al., J. Bacteriol., 297, (1986)) and a gene coding for AKIII (*lysC*, Cassan, M., Parsot, C., Cohen, G.N. and Patte, J.C., J. Biol. Chem., 261, 1052 (1986)) derived from *Escherichia* bacteria have been both revealed, these genes can be obtained by PCR using primers synthesized based on the nucleotide sequences of these genes and chromosome DNA of microorganism such as *E. coli* K-12 or the like as a template. As specific examples, *dapA* and *lysC* derived from *E. coli* will be explained below. However, genes used for the present invention are not limited to them.

15 [0026] It is preferred that DDPS and AK used for the present invention do not suffer feedback inhibition by L-lysine. It has been known that wild-type DDPS derived from *E. coli* suffers feedback inhibition by L-lysine, and that wild-type AKIII derived from *E. coli* suffers suppression and feedback inhibition by L-lysine. Therefore, *dapA* and *lysC* to be introduced into *Methylophilus* bacteria preferably code for DDPS and AKIII having a mutation that desensitizes the feedback inhibition by L-lysine. Hereafter, DDPS having a mutation that desensitizes the feedback inhibition by L-lysine

20 is also referred to as "mutant DDPS", and DNA coding for the mutant DDPS is also referred to as "mutant *dapA*". AKIII derived from *E. coli* having a mutation that desensitizes the feedback inhibition by L-lysine is also referred to as "mutant AKIII", and DNA coding for the mutant AKIII is also referred to as "mutant *lysC*".

[0027] According to the present invention, DDPS and AK are not necessarily required to be a mutant. It has been known that, for example, DDPS derived from *Corynebacterium* bacteria originally does not suffer feedback inhibition

25 by L-lysine.

[0028] A nucleotide sequence of wild-type *dapA* derived from *E. coli* is exemplified by SEQ ID NO: 1. The amino acid sequence of wild-type DDPS coded by said nucleotide sequence is exemplified by SEQ ID NO: 2. A nucleotide sequence of wild-type *lysC* derived from *E. coli* is exemplified by SEQ ID NO: 3. The amino acid sequence of wild-type AKIII coded by said nucleotide sequence is exemplified by SEQ ID NO: 4.

30 [0029] The DNA coding for mutant DDPS that does not suffer feedback inhibition by L-lysine includes a DNA coding for DDPS having the amino acid sequence described in SEQ ID NO: 2 wherein the 118-histidine residue is replaced with a tyrosine residue. The DNA coding for mutant AKIII that does not suffer feedback inhibition by L-lysine includes a DNA coding for AKIII having an amino sequence described in SEQ ID NO: 4 wherein the 352-threonine residue is replaced with an isoleucine residue.

35 [0030] The plasmid used for gene cloning may be any plasmid so long as it can replicate in microorganisms such as *Escherichia* bacteria or the like, and specifically include pBR322, pTWV228, pMW119, pUC19 and so forth.

[0031] The vector that functions in *Methylophilus* bacteria is, for example, a plasmid that can autonomously replicate in *Methylophilus* bacteria. Specifically, there can be mentioned RSF1010, which is a broad host spectrum vector, and derivatives thereof, for example, pAYC32 (Chistorerdov, A.Y., Tsygankov, Y.D. Plasmid, 16, 161-167, (1986)), pMFY42 (Gene, 44, 53, (1990)), pRP301, pTB70 (Nature, 287, 396, (1980)) and so forth.

40 [0032] In order to prepare a recombinant DNA by ligating *dapA* and *lysC* to a vector that functions in *Methylophilus* bacteria, the vector is digested with a restriction enzyme that corresponds to the terminus of DNA fragment containing *dapA* and *lysC*. Ligation is usually performed by using ligase such as T4 DNA ligase. *dapA* and *lysC* may be individually incorporated into separate vectors or into a single vector.

45 [0033] As a plasmid containing a mutant *dapA* coding for mutant DDPS and a mutant *lysC* coding for mutant AKIII, a broad host spectrum plasmid RSFD80 has been known (WO95/16042). *E. coli* JM109 strain transformed with this plasmid was designated as AJ12396, and deposited at National Institute of Bioscience and Human-Technology, Agency of Industrial Science and Technology, Ministry of International Trade and Industry (postal code 305-8566, 1-3 Higashi 1-chome, Tsukuba-shi, Ibaraki-ken, Japan) on October 28, 1993 and received an accession number of FERM P-13936, and it was transferred to an international deposition under the provisions of the Budapest Treaty on November 1, 1994, and received an accession number of FERM BP-4859. RSFD80 can be obtained from the AJ12396 strain in a known manner.

50 [0034] The mutant *dapA* contained in RSFD80 has a nucleotide sequence of wild-type *dapA* of SEQ ID NO: 1 including replacement of C at the nucleotide number 597 with T. The mutant DDPS encoded thereby has an amino acid sequence of SEQ ID NO: 2 including replacement of the 118-histidine residue with a tyrosine residue. The mutant *lysC* contained in RSFD80 has a nucleotide sequence of wild-type *lysC* of SEQ ID NO: 3 including replacement of C at the nucleotide number 1638 with T. The mutant AKIII encoded thereby has an amino acid sequence of SEQ ID NO: 4 including replacement of the 352-threonine residue with an isoleucine residue.

[0035] In order to introduce a recombinant DNA prepared as described above into *Methylophilus* bacteria, any method can be used so long as it provides sufficient transformation efficiency. For example, electroporation can be used (Canadian Journal of Microbiology, 43, 197 (1997)).

[0036] The DDPS activity and/or the AK activity can also be enhanced by the presence of multiple copies of *dapA* and/or *lysC* on chromosome DNA of *Methylophilus* bacteria. In order to introduce multiple copies of *dapA* and/or *lysC* into chromosome DNA of *Methylophilus* bacteria, homologous recombination is performed by using, as a target, a sequence that is present on chromosome DNA of *Methylophilus* bacteria in a multiple copy number. As the sequence present on chromosome DNA in the multiple copy number, a repetitive DNA, inverted repeats present at the end of a transposable element, or the like can be used. Alternatively, as disclosed in Japanese Patent Application Laid-open (Kokai) No. 2-109985/1990, multiple copies of *dapA* and/or *lysC* can be introduced into chromosome DNA by mounting them on a transposon to transfer them. In both of the methods, as a result of increased copy number of *dapA* and/or *lysC* in transformed strains, the DDPS activity and the AK activity should be amplified.

[0037] Besides the above gene amplification, the DDPS activity and/or the AK activity can be amplified by replacing an expression control sequence such as promoters of *dapA* and/or *lysC* with stronger ones (Japanese Patent Application Laid-open (Kokai) No. 1-215280/1989). As such strong promoters, there have been known, for example, *lac* promoter, *trp* promoter, *trc* promoter, *tac* promoter, P_R promoter and P_L promoter of lambda phage, tet promoter, *amyE* promoter, *spac* promoter and so forth. Substitution of these promoters enhances expression of *dapA* and/or *lysC*, and thus the DDPS activity and the AK activity are amplified. Enhancement of expression control sequences can be combined with increase of the copy numbers of *dapA* and/or *lysC*.

[0038] In order to prepare a recombinant DNA by ligating a gene fragment and a vector, the vector is digested with a restriction enzyme corresponding to the terminus of the gene fragment. Ligation is usually performed by ligase such as T4 DNA ligase. As methods for digestion, ligation and others of DNA, preparation of chromosome DNA, PCR, preparation of plasmid DNA, transformation, design of oligonucleotides used as primers and so forth, usual methods well known to those skilled in the art can be used. Such methods are described in Sambrook, J., Fritsch, E. F., and Maniatis, T., "Molecular Cloning: A Laboratory Manual, 2nd Edition", Cold Spring Harbor Laboratory Press, (1989) and so forth.

[0039] In addition to the enhancement of the DDPS activity and/or the AK activity, activity of another enzyme involved in the L-lysine biosynthesis may also be enhanced. Such enzymes include diaminopimelate pathway enzymes such as dihydrodipicolinate reductase, diaminopimelate decarboxylase, diaminopimelate dehydrogenase (WO96/40934 for all of the foregoing enzymes), phosphoenolpyruvate carboxylase (Japanese Patent Application Laid-open (Kokai) No. 60-87788/1985), aspartate aminotransferase (Japanese Patent Publication (Kokoku) No. 6-102028/1994), diaminopimelate epimerase, aspartic acid semialdehyde dehydrogenase and so forth, or aminoadipate pathway enzymes such as homoaconitate hydratase and so forth. Preferably, activity of at least one enzyme of aspartic acid semialdehyde dehydrogenase, dihydrodipicolinate reductase and diaminopimelate decarboxylase is enhanced.

[0040] Aspartokinase, aspartic acid semialdehyde dehydrogenase, dihydrodipicolinate synthase, dihydrodipicolinate reductase and diaminopimelate decarboxylase derived from *Methylophilus methylotrophus* will be described later.

[0041] Further, the microorganisms of the present invention may be decreased in activity of an enzyme that catalyzes a reaction for generating a compound other than L-lysine by branching off from the biosynthetic pathway of L-lysine, or may be deficient in such an enzyme. The enzyme that catalyzes the reaction for generating the compound other than L-lysine by branching off from the biosynthetic pathway L-lysine include homoserine dehydrogenase (see WO95/23864).

[0042] The aforementioned techniques for enhancing activity of an enzyme involved in the L-lysine biosynthesis can be similarly used for other amino acids mentioned below.

[L-Glutamic acid]

[0043] L-Glutamic acid-producing ability can be imparted to *Methylophilus* bacteria by, for example, introducing a DNA that codes for any one of enzymes including glutamate dehydrogenase (Japanese Patent Application Laid-open (Kokai) 61-268185/1986), glutamine synthetase, glutamate synthase, isocitrate dehydrogenase (Japanese Patent Application Laid-open (Kokai) Nos. 62-166890/1987 and 63-214189/1988), aconitate hydratase (Japanese Patent Application Laid-open (Kokai) No. 62-294086/1987), citrate synthase (Japanese Patent Application Laid-open (Kokai) Nos. 62-201585/1987 and 63-119688/1988), phosphoenolpyruvate carboxylase (Japanese Patent Application Laid-open (Kokai) Nos. 60-87788/1985 and 62-55089/1987), pyruvate dehydrogenase, pyruvate kinase, phosphoenolpyruvate synthase, enolase, phosphoglyceromutase, phosphoglycerate kinase, glyceraldehyde-3-phosphate dehydrogenase, triose phosphate isomerase, fructose biphosphate aldolase, phosphofructokinase (Japanese Patent Application Laid-open (Kokai) No. 63-102692/1988), glucose phosphate isomerase, glutamine-oxoglutarate aminotransferase (WO99/07853) and so forth.

[0044] Further, the microorganisms of the present invention may be decreased in activity of an enzyme that catalyzes

a reaction for generating a compound other than L-glutamic acid by branching off from the biosynthetic pathway of L-glutamic acid, or may be deficient in such an enzyme. The enzyme that catalyzes the reaction for generating the compound other than L-glutamic acid by branching off from the biosynthetic pathway L-glutamic acid include α -ketoglutarate dehydrogenase (α KGDH), isocitrate lyase, phosphate acetyltransferase, acetate kinase, acetohydroxy acid synthase, acetolactate synthase, formate acetyltransferase, lactate dehydrogenase, glutamate decarboxylase, 1-pyrroline dehydrogenase and so forth.

[L-Threonine]

[0045] L-Threonine-producing ability can be imparted or enhanced by, for example, enhancing activities of aspartokinase, homoserine dehydrogenase, homoserine kinase and threonine synthase. The activities of these enzymes can be enhanced by, for example, transforming *Methylophilus* bacteria using a recombinant plasmid containing a threonine operon (Japanese Patent Application Laid-open (Kokai) Nos. 55-131397/1980, 59-31691/1984 and 56-15696/1981 and Japanese Patent Application Laid-open (Kohyo) No. 3-501682/1991).

[0046] The production ability can also be imparted or enhanced by amplifying or introducing a threonine operon having a gene coding for aspartokinase of which feedback inhibition by L-threonine is desensitized (Japanese Patent Publication (Kokoku) No. 1-29559/1989), a gene coding for homoserine dehydrogenase (Japanese Patent Application Laid-open (Kokai) No. 60-012995/1985) or a gene coding for homoserine kinase and homoserine dehydrogenase (Japanese Patent Application Laid-open (Kokai) No. 61-195695/1986).

[0047] Further, L-threonine-producing ability can be improved by introducing a DNA coding for a mutant phosphoenolpyruvate carboxylase having a mutation for desensitizing feedback inhibition by aspartic acid.

[L-Valine]

[0048] L-Valine-producing ability can be imparted by, for example, introducing into *Methylophilus* bacteria an L-valine biosynthesis gene whose control mechanism has been substantially desensitized. There may also be introduced a mutation that substantially desensitizes a control mechanism of an L-valine biosynthesis gene carried by a microorganism belonging to the genus *Methylophilus*.

[0049] Examples of the L-valine biosynthesis gene include, for example, the *ilvGMEDA* operon of *E. coli*. Threonine deaminase encoded by an *ilvA* gene catalyzes the deamination reaction converting L-threonine into 2-ketobutyric acid, which is the rate-determining step of L-isoleucine biosynthesis. Therefore, in order to attain efficient progression of the L-valine synthesis reactions, it is preferable to use an operon that does not express threonine deaminase activity. Examples of the *ilvGMEDA* operon that does not express such threonine deaminase activity include an *ilvGMEDA* operon wherein a mutation for eliminating threonine deaminase activity is introduced into *ilvA*, or *ilvA* is disrupted, and an *ilvGMED* operon wherein *ilvA* is deleted.

[0050] Since the *ilvGMEDA* operon suffers expression control of operon (attenuation) by L-valine and/or L-isoleucine and/or L-leucine, the region required for the attenuation is preferably removed or mutated to desensitize the suppression of expression by L-valine.

[0051] An *ilvGMEDA* operon which does not express threonine deaminase activity and in which attenuation is desensitized as described above can be obtained by subjecting a wild-type *ilvGMEDA* operon to a mutagenesis treatment or modifying it by means of gene recombination techniques (see WO96/06926).

[L-Leucine]

[0052] L-Leucine-producing ability is imparted or enhanced by, for example, introducing into a microorganism belonging to the genus *Methylophilus* an L-leucine biosynthesis gene whose control mechanism has been substantially desensitized, in addition to the above characteristics required for the production of L-valine. It is also possible to introduce such a mutation that the control mechanism of an L-leucine biosynthesis gene in a microorganism belonging to the genus *Methylophilus* should be substantially eliminated. Examples of such a gene include, for example, an *leuA* gene which provides an enzyme in which inhibition by L-leucine is substantially eliminated.

[L-Isoleucine]

[0053] L-Isoleucine-producing ability can be imparted by, for example, introducing a *thrABC* operon containing a *thrA* gene coding for aspartokinase I/homoserine dehydrogenase I derived from *E. coli* wherein inhibition by L-threonine has been substantially desensitized and an *ilvGMEDA* operon which contains an *ilvA* gene coding for threonine deaminase wherein inhibition by L-isoleucine is substantially desensitized and whose region required for attenuation is removed (Japanese Patent Application Laid-open (Kokai) No. 8-47397/1996).

[Other amino acids]

[0054] Biosyntheses of L-tryptophan, L-phenylalanine, L-tyrosine, L-threonine and L-isoleucine can be enhanced by increasing phosphoenolpyruvate-producing ability of *Methylophilus* bacteria (WO97/08333).

5 [0055] The production abilities for L-phenylalanine and L-tyrosine are improved by amplifying or introducing a desensitized chorismate mutase-prephenate dehydratase (CM-PDT) gene (Japanese Patent Application Laid-open (Kokai) Nos. 5-236947/1993 and 62-130693/1987) and a desensitized 3-deoxy-D-arabinoheptulonate-7-phosphate synthase (DS) gene (Japanese Patent Application Laid-open (Kokai) Nos. 5-236947/1993 and 61-124375/1986).

10 [0056] The producing ability of L-tryptophan is improved by amplifying or introducing a tryptophan operon containing a gene coding for desensitized anthranilate synthase (Japanese Patent Application Laid-open (Kokai) Nos. 57-71397/1982, 62-244382/1987 and US Patent No. 4,371,614).

[0057] In the present specification, the expression that enzyme "activity is enhanced" usually refers to that the intracellular activity of the enzyme is higher than that of a wild type strain, and when a strain in which the activity of the enzyme is enhanced is obtained by modification using gene recombinant techniques or the like, the intracellular activity of the enzyme is higher than that of the strain before the modification. The expression that enzyme "activity is decreased" usually refers to that the intracellular activity of the enzyme is lower than that of a wild type strain, and when a strain in which the activity of the enzyme is decreased is obtained by modification using gene recombinant techniques or the like, the intracellular activity of the enzyme is lower than that of the strain before the modification.

20 [0058] L-Amino acids can be produced by culturing *Methylophilus* bacteria having L-amino acid-producing ability obtained as described above in a medium to produce and accumulate L-amino acids in the culture, and collecting the L-amino acids from the culture.

[0059] Bacterial cells of *Methylophilus* bacteria with an increased L-amino acid content compared with wild strains of *Methylophilus* bacteria can be produced by culturing *Methylophilus* bacteria having L-amino acid-producing ability in a medium to produce and accumulate L-amino acids in bacterial cells of the bacteria.

25 [0060] Microorganisms used for the present invention can be cultured by methods usually used for culturing microorganisms having methanol-assimilating property. The medium used for the present invention may be a natural or synthetic medium so long as it contains a carbon source, a nitrogen source, inorganic ions and other trace amount organic constituents as required.

30 [0061] By using methanol as a main carbon source, L-amino acids can be prepared at a low cost. When methanol is used as a main carbon source, it is usually added to a medium in an amount of 0.001 to 30%. As the nitrogen source, ammonium sulfate or the like is used by adding it to the medium. Other than these, there are usually added small amounts of the trace amount constituents such as potassium phosphate, sodium phosphate, magnesium sulfate, ferrous sulfate and manganese sulfate.

35 [0062] The culture is usually performed under an aerobic condition obtained by, for example, shaking or stirring for aeration, at pH 5 to 9 and a temperature of 20 to 45°C, and it is usually completed within 24 to 120 hours.

[0063] Collection of L-amino acids from culture can be usually attained by a combination of known methods such as those using ion exchange resin, precipitation and others.

[0064] Further, *Methylophilus* bacterium cells can be separated from the medium by usual methods for separating microbial cells.

40

<2> Gene of the present invention

[0065] The DNA of the present invention is a gene which codes for one of the enzymes, aspartokinase (henceforth also abbreviated as "AK"), aspartic acid semialdehyde dehydrogenase (henceforth also abbreviated as "ASD"), dihydrodipicolinate synthase (henceforth also abbreviated as "DDPS"), dihydrodipicolinate reductase (henceforth also abbreviated as "DDPR"), and diaminopimelate decarboxylase (henceforth also abbreviated as "DPDC") derived from *Methylophilus methylotrophus*.

45 [0066] The DNA of the present invention can be obtained by, for example, transforming a mutant strain of a microorganism deficient in AK, ASD, DDPS, DDPR or DPDC using a gene library of *Methylophilus methylotrophus*, and selecting a clone in which auxotrophy is recovered.

50 [0067] A gene library of *Methylophilus methylotrophus* can be produced as follows, for example. First, total chromosome DNA is prepared from a *Methylophilus methylotrophus* wild strain, for example, the *Methylophilus methylotrophus* AS1 strain (NCIMB10515), by the method of Saito et al. (Saito, H. and Miura, K., Biochem. Biophys. Acta 72, 619-629, (1963)) or the like, and partially digested with a suitable restriction enzyme, for example, *Sau3AI* or *AluI*, to obtain a mixture of various fragments. By controlling the degree of the digestion through adjustment of digestion reaction time and so forth, a wide range of restriction enzymes can be used.

55 [0068] Subsequently, the digested chromosome DNA fragments are ligated to vector DNA autonomously replicable in *Escherichia coli* cells to produce recombinant DNA. Specifically, a restriction enzyme producing the same terminal

nucleotide sequence as that produced by the restriction enzyme used for the digestion of chromosome DNA is allowed to act on the vector DNA to fully digest and cleave the vector. Then, the mixture of chromosome DNA fragments and the digested and cleaved vector DNA are mixed, and a ligase, preferably T4 DNA ligase, is allowed to act on the mixture to obtain recombinant DNA.

5 [0069] A gene library solution can be obtained by transforming *Escherichia coli*, for example, the *Escherichia coli* JM109 strain or the like, using the obtained recombinant DNA, and preparing recombinant DNA from the culture broth of the transformant. This transformation can be performed by the method of D.M. Morrison (Methods in Enzymology 68, 326 (1979)), the method of treating recipient cells with calcium chloride so as to increase the permeability of DNA (Mandel, M. and Higa, A., J. Mol. Biol., 53, 159 (1970)) and so forth. In the examples mentioned hereinafter, electro-

10 poration was used.
[0070] As examples of the aforementioned vector, there can be mentioned pUC19, pUC18, pUC118, pUC119, pBR322, pHSG299, pHSG298, pHSG399, pHSG398, RSF1010, pMW119, pMW118, pMW219, pMW218, pSTV28, pSTV29 and so forth. Phage vectors can also be used. Since pUC118 and pUC119 contain an ampicillin resistance gene, and pSTV28 and pSTV29 contain a chloramphenicol resistance gene, for example, only transformants which harbor a vector or a recombinant DNA can be grown by using a medium containing ampicillin or chloramphenicol.

15 [0071] As the method for culturing the transformants and collecting recombinant DNA from bacterial cells, the alkali SDS method and the like can be mentioned.

[0072] A mutant microbial strain deficient in AK, ASD, DDPS, DDPB or DPDC is transformed by using the gene library solution of *Methylophilus methylotrophus* obtained as described above, and clones whose auxotrophy is recovered are selected.

20 [0073] Examples of a mutant microbial strain deficient in AK include *E. coli* GT3 deficient in three kinds of genes coding for AK (*thrA*, *metLM*, *lysC*). Examples of a mutant microbial strain deficient in ASD include *E. coli* Hfr3000 U482 (CGSC 5081 strain). Examples of a mutant microbial strain deficient in DDPS include *E. coli* AT997 (CGSC 4547 strain). Examples of a mutant microbial strain deficient in DDPB include *E. coli* AT999 (CGSC 4549 strain). Examples of a mutant microbial strain deficient in DPDC include *E. coli* AT2453 (CGSC 4505 strain). These mutant strains can be obtained from *E. coli* Genetic Stock Center (the Yale University, Department of Biology, Osborn Memorial Labs., P.O. Box 6666, New Haven 06511-7444, Connecticut, U.S.).

25 [0074] Although all of the aforementioned mutant strains cannot grow in M9 minimal medium, transformant strains which contain a gene coding for AK, ASD, DDPS, DDPB or DPDC can grow in M9 minimal medium because these genes function in the transformants. Therefore, by selecting transformant strains that can grow in the minimal medium and collecting recombinant DNA from the strains, DNA fragments containing a gene that codes for each enzyme can be obtained. *E. coli* AT999 (CGSC 4549 strain) shows extremely slow growth rate even in a complete medium such as L medium when diaminopimelic acid is not added to the medium. However, normal growth can be observed for its transformant strains which contain a gene coding for DDPB derived from *Methylophilus methylotrophus*, because of the function of the gene. Therefore, a transformant strain that contains a gene coding for DDPB can also be obtained by selecting a transformant strain normally grown in L medium.

30 [0075] By extracting an insert DNA fragment from the obtained recombinant DNA and determining its nucleotide sequence, an amino acid sequence of each enzyme and nucleotide sequence of the gene coding for it can be determined.

40 [0076] The gene coding for AK of the present invention (henceforth also referred to "ask") codes for AK which has the amino acid sequence of SEQ ID NO: 6 shown in Sequence Listing. As a specific example of the ask gene, there can be mentioned a DNA having the nucleotide sequence which consists of nucleotides of SEQ ID NO: 5. The ask gene of the present invention may have a sequence in which codon corresponding to each of the amino acids is replaced with equivalent codon so long as it codes for the same amino acid sequence as the amino acid sequence of SEQ ID NO: 6.

45 [0077] The gene which codes for ASD of the present invention (henceforth also referred to as "asd") codes for ASD which has the amino acid sequence of SEQ ID NO: 8 shown in Sequence Listing. As a specific example of the asd gene, a DNA which contains the nucleotide sequence consisting of the nucleotides of the nucleotide numbers 98-1207 in SEQ ID NO: 7 can be mentioned. The asd gene of the present invention may have a sequence in which codon corresponding to each of the amino acids is replaced with equivalent codon so long as it codes for the same amino acid sequence as the amino acid sequence of SEQ ID NO: 8.

50 [0078] The gene which codes for DDPS of the present invention (henceforth also referred to as "dapA") codes for DDPS which has the amino acid sequence of SEQ ID NO: 10 shown in Sequence Listing. As a specific example of the dapA gene, a DNA which has the nucleotide sequence consisting of the nucleotides of the nucleotide numbers 1268-2155 in SEQ ID NO: 9 can be mentioned. The dapA gene of the present invention may have a sequence in which codon corresponding to each of the amino acids is replaced with equivalent codon so long as it codes for the same amino acid sequence as the amino acid sequence of SEQ ID NO: 10.

55 [0079] The gene which codes for DDBB of the present invention (henceforth also referred to as "dapB") codes for

DDBR which has the amino acid sequence of SEQ ID NO: 12 shown in Sequence Listing. As a specific example of the *dapB* gene, a DNA which has the nucleotide sequence consisting of the nucleotides of the nucleotide numbers 2080-2883 in SEQ ID NO: 11 can be mentioned. The *dapB* gene of the present invention may have a sequence in which codon corresponding to each of the amino acids is replaced with equivalent codon so long as it codes for the same amino acid sequence as the amino acid sequence of SEQ ID NO: 12.

[0080] The gene which codes for DPDC of the present invention (henceforth also referred to as "*lysA*") codes for DPDC which has the amino acid sequence of SEQ ID NO: 14 shown in Sequence Listing. As a specific example of the *lysA* gene, a DNA which has the nucleotide sequence consisting of the nucleotides of the nucleotide numbers 751-1995 in SEQ ID NO: 13 can be mentioned. The *lysA* gene of the present invention may have a sequence in which codon corresponding to each of the amino acids is replaced with equivalent codon so long as it codes for the same amino acid sequence as the amino acid sequence of SEQ ID NO: 14.

[0081] The gene for each enzyme of the present invention may have an amino acid sequence corresponding to each amino acid sequence of SEQ ID NO: 6, 8, 10, 12 or 14 including substitution, deletion, insertion, addition or inversion of one or several amino acids, and may code a protein having activity of AK, ASD, DDPS, DDPR or DPDC. The expression "one or several" used herein preferably means a number of 1 to 10, more preferably a number of 1 to 5, more preferably a number of 1 to 2.

[0082] The DNA which codes for the substantially same protein as AK, ASD, DDPS, DDPR or DPDC such as those mentioned above can be obtained by modifying each nucleotide sequence so that the amino acid sequence should contain substitution, deletion, insertion, addition or inversion of an amino acid residue or residues at a particular site by, for example, site-specific mutagenesis. Such a modified DNA as mentioned above may also be obtained by a conventional mutagenesis treatment. Examples of the mutagenesis treatment include in vitro treatment of DNA coding for AK, ASD, DDPS, DDPR or DPDC with hydroxylamine or the like, treatment of a microorganism such as *Escherichia* bacteria containing a gene coding for AK, ASD, DDPS, DDPR or DPDC by UV irradiation or with mutagenesis agents used for usual mutagenesis treatment such as N-methyl-N'-nitro-N-nitrosoguanidine (NTG) and nitrous acid.

[0083] The aforementioned substitution, deletion, insertion, addition or inversion of nucleotides includes naturally occurring mutations (mutant or variant) such as those observed depending difference between species or strains of microorganisms containing AK, ASD, DDPS, DDPR or DPDC and so forth.

[0084] The DNA which codes for substantially the same protein as AK, ASD, DDPS, DDPR or DPDC can be obtained by allowing expression of a DNA having such a mutation as mentioned above in a suitable cell, and examining AK, ASD, DDPS, DDPR or DPDC activity of the expression product. The DNA which codes for substantially the same protein as AK, ASD, DDPS, DDPR or DPDC can also be obtained by isolating, from DNAs coding for AK, ASD, DDPS, DDPR or DPDC which have mutations or cells containing each of them, a DNA hybridizable with a probe containing a nucleotide sequence comprising the nucleotide sequence of the nucleotide numbers 510-1736 of SEQ ID NO: 5, a nucleotide sequence comprising the nucleotide sequence of the nucleotide numbers 98-1207 of SEQ ID NO: 7, a nucleotide sequence comprising the nucleotide sequence of the nucleotide numbers 1268-2155 of SEQ ID NO: 9, a nucleotide sequence comprising the nucleotide sequence of the nucleotide numbers 2080-2883 of SEQ ID NO: 11, or a nucleotide sequence comprising the nucleotide sequence of the nucleotide numbers 751-1995 of SEQ ID NO: 13, or a part of those nucleotide sequences under a stringent condition, and coding for a protein having AK, ASD, DDPS, DDPR or DPDC activity. In the present specification, to have a nucleotide sequence or a part thereof means to have the nucleotide sequence or the part thereof, or a nucleotide complementary thereto.

[0085] The term "stringent condition" used herein means a condition that allows formation of so-called specific hybrid and does not allow formation of non-specific hybrid. This condition may vary depending on the nucleotide sequence and length of the probe. However, it may be, for example, a condition that allows hybridization of highly homologous DNA such as DNA having homology of 40% or higher, but does not allow hybridization of DNA of lower homology than defined above, or a condition that allows hybridization under a washing condition of usual Southern hybridization, of a temperature of 60°C and salt concentrations corresponding to 1 x SSC and 0.1% SDS, preferably 0.1 x SSC and 0.1% SDS.

[0086] A partial sequence of each gene can also be used as the probe. Such a probe can be produced by PCR (polymerase chain reaction) using oligonucleotides produced based on a nucleotide sequence of each gene as primers and a DNA fragment containing each gene as a template. When a DNA fragment having a length of about 300 bp is used as the probe, washing condition for hybridization may be, for example, 50°C, 2 x SSC and 0.1% SDS.

[0087] Genes that hybridize under such a condition as mentioned above also include those having a stop codon occurring in its sequence and those encoding an enzyme no longer having its activity due to a mutation of active center. However, such genes can readily be eliminated by ligating the genes to a commercially available activity expression vector, and measuring AK, ASD, DDPS, DDPR or DPDC activity.

[0088] Since the nucleotide sequences of the genes that codes for AK, ASD, DDPS, DDPR and DPDC derived from *Methylophilus methylotrophus* were revealed by the present invention, DNA sequences which code for AK, ASD, DDPS, DDPR and DPDC can be obtained from a *Methylophilus methylotrophus* gene library by hybridization using oligonu-

cleotide probes produced based on the sequences. Moreover, DNA sequences which code for these enzymes can also be obtained by amplifying them from *Methylophilus methylotrophus* chromosome DNA by PCR using oligonucleotide primers produced based on the aforementioned nucleotide sequences.

[0089] The aforementioned genes can suitably be utilized to enhance L-lysine-producing ability of *Methylophilus* bacteria.

EXAMPLES

[0090] The present invention will further specifically be explained with reference to the following examples hereafter.

[0091] The reagents used were obtained from Wako Pure Chemicals or Nakarai Tesque unless otherwise indicated. The compositions of the media used in each example are shown below. pH was adjusted with NaOH or HCl for all media.

(L medium)	
Bacto trypton (DIFCO)	10 g/L
Yeast extract (DIFCO)	5 g/L
NaCl	5 g/L
[steam-sterilized at 120°C for 20 minutes]	

(L agar medium)	
L medium	
Bacto agar (DIFCO)	15 g/L
[steam-sterilized at 120°C for 20 minutes]	

(SOC medium)	
Bacto trypton (DIFCO)	20 g/L
Yeast extract (DIFCO)	5 g/L
10 mM NaCl	
2.5 mM KCl	
10 mM MgSO ₄	
10 mM MgCl ₂	
20 mM Glucose	

[The constituents except for magnesium solution and glucose were steam-sterilized (120°C, 20 minutes), then 2 M magnesium stock solution (1 M MgSO₄, 1 M MgCl₂) and 2 M glucose solution, which solutions had been passed through a 0.22-μm filter, were added thereto, and the mixture was passed through a 0.22-μm filter again.]

(121M1 medium)	
K ₂ HPO ₄	1.2 g/L
KH ₂ PO ₄	0.62 g/L
NaCl	0.1 g/L
(NH ₄) ₂ SO ₄	0.5 g/L
MgSO ₄ •7H ₂ O	0.2 g/L
CaCl ₂ •6H ₂ O	0.05 g/L
FeCl ₃ •6H ₂ O	1.0 mg/L
H ₃ BO ₃	10 μg/L
CuSO ₄ •5H ₂ O	5 μg/L
MnSO ₄ •5H ₂ O	10 μg/L
ZnSO ₄ •7H ₂ O	70 μg/L
NaMoO ₄ •2H ₂ O	10 μg/L

EP 1 188 822 A1

(continued)

(121M1 medium)	
CoCl ₂ •6H ₂ O	5 µg/L
Methanol 1% (vol/vol), pH 7.0	

[The constituents except for methanol were steam-sterilized at 121°C for 15 minutes. After the constituents sufficiently cooled, methanol was added.]

(Composition of 121 production medium)	
Methanol	2%
Dipotassium phosphate	0.12%
Potassium phosphate	0.062%
Calcium chloride hexahydrate	0.005%
Magnesium sulfate heptahydrate	0.02%
Sodium chloride	0.01%
Ferric chloride hexahydrate	1.0 mg/L
Ammonium sulfate	0.3%
Cupric sulfate pentahydrate	5 µg/L
Manganous sulfate pentahydrate	10 µg/L
Sodium molybdate dihydrate	10 µg/L
Boric acid	10 µg/L
Zinc sulfate heptahydrate	70 µg/L
Cobaltous chloride hexahydrate	5 µg/L
Calcium carbonate (Kanto Kagaku)	3%
(pH 7.0)	

(121M1 Agar medium)	
121M1 medium	
Bacto agar (DIFCO)	15 g/L

[The constituents except for methanol were steam-sterilized at 121°C for 15 minutes. After the constituents sufficiently cooled, methanol was added.]

(M9 minimal medium)	
Na ₂ HPO ₄ •12H ₂ O	16 g/L
KH ₂ PO ₄	3 g/L
NaCl	0.5 g/L
NH ₄ Cl	1 g/L
MgSO ₄ •7H ₂ O	246.48 mg/L
Glucose	2 g/L
pH 7.0	

[MgSO₄ and glucose were separately sterilized (120°C, 20 minutes) and added. A suitable amount of amino acids and vitamins were added as required.]

(M9 minimal agar medium)	
M9 minimal medium	
Bacto agar (DIFCO)	15 g/L

Example 1

Creation of L-lysine-producing bacterium (1)

5 (1) Introduction of mutant *lysC* and mutant *dapA* into *Methylophilus* bacterium

[0092] A mutant *lysC* and a mutant *dapA* were introduced into a *Methylophilus* bacterium by using a known plasmid RSFD80 (see WO95/16042) containing them. RSFD80 is a plasmid pVIC40 (International Publication WO90/04636, Japanese Patent Application Laid-open (Kohyo) No. 3-501682/1991) derived from a broad host spectrum vector plasmid pAYC32 (Chistorerdov, A.Y., Tsygankov, Y.D., Plasmid, 16, 161-167, (1986)), which is a derivative of RSF1010, in which a mutant *dapA* and a mutant *lysC* derived from *E. coli* are located in this order downstream of the promoter (tetP) of the tetracycline resistance gene of pVIC40 so that the transcription directions of the genes are ordinary with respect to tetP. The mutant *dapA* coded for a mutant DDPS in which the 118-histidine residue was replaced with a tyrosine residue. The mutant *lysC* coded for a mutant AKIII in which the 352-threonine residue was replaced with an isoleucine residue.

[0093] RSFD80 was constructed as follows. The mutant *dapA* on a plasmid pdapAS24 was ligated to pVIC40 at a position downstream of the promoter of the tetracycline resistance gene to obtain RSF24P as shown in Fig. 1. Then, the plasmid RSFD80 which had the mutant *dapA* and a mutant *lysC* was prepared from RSF24P and pLLC*80 containing the mutant *lysC* as shown in Fig. 2. That is, while pVIC40 contains a threonine operon, this threonine operon is replaced with a DNA fragment containing the mutant *dapA* and a DNA fragment containing the mutant *lysC* in RSFD80.

[0094] The *E. coli* JM109 strain transformed with the RSFD80 plasmid was designated as AJ12396, and deposited at National Institute of Bioscience and Human-Technology, Agency of Industrial Science and Technology, Ministry of International Trade and Industry (postal code 305-8566, 1-3 Higashi 1-chome, Tsukuba-shi, Ibaraki-ken, Japan) on October 28, 1993 and received an accession number of FERM P-13936, and it was transferred to an international deposition under the provisions of the Budapest Treaty on November 1, 1994, and received an accession number of FERM BP-4859.

[0095] The *E. coli* AJ1239 strain was cultured in 30 ml of LB medium containing 20 mg/L of streptomycin at 30°C for 12 hours, and the RSFD80 plasmid was purified from the obtained cells by using Wizard® Plus Midipreps DNA Purification System (sold by Promega).

[0096] The RSFD80 plasmid produced as described above was introduced into the *Methylophilus methylotrophus* AS1 strain (NCIMB10515) by electroporation (Canadian Journal of Microbiology, 43, 197 (1997)). As a control, a DNA region coding for the threonine operon was deleted from the pVIC40 plasmid used for producing the RSFD80 plasmid to produce a pRS plasmid comprising only the vector region (see Japanese Patent Application Laid-open (Kohyo) No. 3-501682/1991), and the pRS plasmid was introduced into the AS1 strain in the same manner as that used for RSFD80.

(2) AKIII Activity of *Methylophilus* bacterium containing mutant *lysC* and mutant *dapA* derived from *E. coli*

[0097] Cell-free extracts were prepared from the *Methylophilus methylotrophus* AS1 strain containing the RSFD80 plasmid (also referred to as "AS1/RSFD80" hereinafter) and the *Methylophilus methylotrophus* AS1 strain containing the pRS plasmid (also referred to as "AS1/pRS" hereinafter), and AK activity was measured. The cell-free extracts (crude enzyme solutions) were prepared as follows. The AS1/RSFD80 strain and AS1/pRS strain were each inoculated to 121 production medium of the above composition containing 20 mg/L of streptomycin, cultured at 37°C for 34 hours with shaking, and then calcium carbonate was removed and cells were harvested.

[0098] The bacterial cells obtained as described above were washed with 0.2% KCl under a condition of 0°C, suspended in 20 mM potassium phosphate buffer (pH 7) containing 10 mM MgSO₄, 0.8 M (NH₄)₂SO₄ and 0.03 M β-mercaptoethanol, and disrupted by sonication (0°C, 200 W, 10 minutes). The sonicated cell suspension was centrifuged at 33,000 rpm for 30 minutes under a condition of 0°C, and the supernatant was separated. To the supernatant, ammonium sulfate was added to 80% saturation, and the mixture was left at 0°C for 1 hour, and centrifuged. The pellet was dissolved in 20 mM potassium phosphate buffer (pH 7) containing 10 mM MgSO₄, 0.8 M (NH₄)₂SO₄ and 0.03 M β-mercaptoethanol.

[0099] The measurement of AK activity was performed in accordance with the method of Stadtman (Stadtman, E. R., Cohen, G.N., LeBras, G., and Robichon-Szulmajster, H., J. Biol. Chem., 236, 2033 (1961)). That is, a reaction solution of the following composition was incubated at 30°C for 45 minutes, and color development was caused by adding a FeCl₃ solution (2.8 N HCl: 0.4 ml, 12% TCA: 0.4 ml, 5% FeCl₃·6H₂O/0.1 N HCl: 0.7 ml). The reaction solution was centrifuged, and absorbance of the supernatant was measured at 540 nm. The activity was represented in terms of the amount of hydroxamic acid produced in 1 minute (1 U = 1 μmol/minute). The molar extinction coefficient was set to be 600. The reaction solution not containing potassium aspartate was used as a blank. When the enzymatic

activity was measured, L-lysine was added to the enzymatic reaction solution at various concentrations to examine degree of inhibition by L-lysine. The results are shown in Table 1.

(Composition of reaction solution)	
Reaction mixture *1	0.3 ml
Hydroxylamine solution *2	0.2 ml
0.1 M Potassium aspartate (pH 7.0)	0.2 ml
Enzyme solution	0.1 ml
Water (balance)	Total 1 ml

*1: 1 M Tris-HCl (pH 8.1): 9 ml, 0.3 M MgSO₄: 0.5 ml and 0.2 M ATP (pH 7.0): 5 ml

*2: 8 M Hydroxylamine solution neutralized with KOH immediately before use

Table 1

Strain	AK activity (Specific activity*1)	Specific activity with 5 mM L-lysine	Desensitization degree of inhibition*2 (%)
AS1/pRS	7.93	9.07	114
AS1/RSFD80	13.36	15.33	115

*1: nmol/minute/mg protein

*2: Activity retention ratio in the presence of 5 mM LERR-lysine

[0100] As shown in Table 1, AK activity was increased by about 1.7 times by the introduction of the RSFD80 plasmid. Further, it was confirmed that the inhibition by L-lysine was completely desensitized in AK derived from *E. coli* that was encoded by the RSFD80 plasmid. Moreover, it was found that AK that was originally retained by the AS1 strain was not inhibited by L-lysine alone. The inventors of the present invention have discovered that the AK derived from the AS1 strain was inhibited by 100% when 2 mM for each of L-lysine and L-threonine were present in the reaction solution (concerted inhibition).

(3) Production of L-lysine by *Methylophilus* bacterium containing mutant *lysC* and mutant *dapA* derived from *E. coli*

[0101] Then, the AS1/RSFD80 strain and the AS1/pRS strain were inoculated to 121 production medium containing 20 mg/L of streptomycin, and cultured at 37°C for 34 hours with shaking. After the culture was completed, the bacterial cells and calcium carbonate were removed by centrifugation, and L-lysine concentration in the culture supernatant was measured by an amino acid analyzer (JASCO Corporation [Nihon Bunko], high performance liquid chromatography). The results are shown in Table 2.

Table 2

Strain	Production amount of L-lysine hydrochloride (g/L)
AS1/pRS	0
AS1/RSFD80	0.3

Example 2

Creation of L-lysine-producing bacterium (2)

(1) Introduction of *tac* promoter region into broad host spectrum vector

[0102] In order to produce a large amount of enzyme involved in the biosynthesis of L-lysine (Lys) in *Methylophilus methylotrophus*, *tac* promoter was used for gene expression of the target enzyme. The promoter is frequently used in *E. coli*.

[0103] The *tac* promoter region was obtained by amplification through PCR using DNA of pKK233-3 (Pharmacia) as a template, DNA fragments having the nucleotide sequences of SEQ ID NOS: 15 and 16 as primers, and a heat-resistant DNA polymerase. The PCR was performed with a cycle of 94°C for 20 seconds, 60°C for 30 seconds, and 72°C for 60 seconds, which was repeated 30 times. Then, the amplified DNA fragment was collected and treated with

restriction enzymes *EcoRI* and *PstI*. On the other hand, a broad host spectrum vector pRS (see Japanese Patent Application Laid-open (Kohyo) No. 3-501682/1991) was also digested with the same restriction enzymes, and the aforementioned DNA fragment which contained the *tac* promoter region was introduced into the restriction enzyme digestion termini to construct pRS-*tac*.

(2) Preparation of *dapA* gene (dihydrodipicolinate synthase gene) expression plasmid pRS-*dapA24* and *lysC* gene (aspartokinase gene) expression plasmid pRS-*lysC80*

[0104] A mutant gene (*dapA**24) coding for dihydrodipicolinate synthase whose feedback inhibition for the enzyme activity by Lys was partially desensitized was introduced into the plasmid pRS-*tac* which was prepared by the method described in the above (1).

[0105] First, the *dapA**24 gene region was obtained by amplification through PCR using DNA of RSFD80 (see Example 1) as a template, and DNA fragments having the nucleotide sequences of SEQ ID NOS: 17 and 18 as primers. The PCR was performed with a cycle of 94°C for 20 seconds, 60°C for 30 seconds, and 72°C for 90 seconds, which was repeated 30 times. Then, the fragment was treated with restriction enzymes *Sse8387I* and *XbaI* to prepare a *dapA**24 gene fragment having corresponding cleaved termini. On the other hand, pRS-*tac* was also treated with *Sse8387I* and partially digested with *XbaI* in the same manner as described above. To this digested plasmid, the aforementioned *dapA**24 gene fragment was ligated by using T4 ligase to obtain pRS-*dapA24*.

[0106] Similarly, a gene (*lysC**80) coding for aspartokinase whose feedback inhibition for the enzyme activity by Lys was partially desensitized was obtained by PCR using DNA of RSFD80 as a template, and DNA fragments having the nucleotide sequences of SEQ ID NOS: 19 and 20 as primers. The PCR was performed with a cycle of 94°C for 20 seconds, 60°C for 30 seconds, and 72°C for 90 seconds, which was repeated 30 times. Then, the obtained DNA fragment was treated with restriction enzymes *Sse8387I* and *SapI*. On the other hand, the vector pRS-*tac* was also treated with *Sse8387I* and *SapI*. To this digested plasmid, the aforementioned *lysC**80 gene fragment was ligated by using T4 ligase to obtain pRS-*lysC80*.

(3) Introduction of pRS-*dapA24* or pRS-*lysC80* into *Methylophilus methylotrophus* and evaluation of culture

[0107] Each of pRS-*dapA24* and pRS-*lysC80* obtained as described above was introduced into the *Methylophilus methylotrophus* AS1 strain (NCIMB10515) by electroporation to obtain AS1/pRS-*dapA24* and AS1/pRS-*lysC80*, respectively. Each strain was inoculated to 121 production medium containing 20 mg/L of streptomycin, and cultured at 37°C for 48 hours with shaking. As a control strain, AS1 strain harboring pRS was also cultured in a similar manner. After the culture was completed, the cells and calcium carbonate were removed by centrifugation, and L-lysine concentration in the culture supernatant was measured by an amino acid analyzer (JASCO Corporation [Nihon Bunko], high performance liquid chromatography). The results are shown in Table 3.

Table 3

Strain	Production amount of L-lysine hydrochloride (g/L)
AS1/pRS	<0.01
AS1/pRS- <i>lysC80</i>	0.06
AS1/pRS- <i>dapA24</i>	0.13

Example 3

Creation of L-lysine-producing bacterium (3)

[0108] The *Methylophilus methylotrophus* AS1 strain (NCIMB10515) was inoculated to 121M1 medium and cultured at 37°C for 15 hours. The obtained bacterial cells were treated with NTG in a conventional manner (NTG concentration: 100 mg/L, 37°C, 5 minutes), and spread onto 121M1 agar medium containing 7 g/L of S-(2-aminoethyl)-cysteine (AEC) and 3 g/L of L-threonine. The cells were cultured at 37°C for 2 to 8 days, and the formed colonies were picked up to obtain AEC-resistant strains.

[0109] The aforementioned AEC-resistant strains were inoculated to 121 production medium, and cultured at 37°C for 38 hours under an aerobic condition. After the culture was completed, the cells and calcium carbonate were removed from the medium by centrifugation, and L-lysine concentration in the culture supernatant was measured by an amino acid analyzer (JASCO Corporation [Nihon Bunko], high performance liquid chromatography). A strain showing improved L-lysine-producing ability compared with the parent strain was selected, and designated as *Methylophilus meth-*

tylotrophus AR-166 strain. The L-lysine production amounts of the parent strain (AS1 strain) and the AR-166 strain are shown in Table 4.

Table 4

Strain	Production amount of L-lysine hydrochloride (mg/L)
AS1	5.8
AR-166	80

[0110] The *Methylophilus methylotrophus* AR-166 strain was given a private number of AJ13608, and was deposited at National Institute of Bioscience and Human-Technology, Agency of Industrial Science and Technology, Ministry of International Trade and Industry (postal code 305-8566, 1-3 Higashi 1-chome, Tsukuba-shi, Ibaraki-ken, Japan) on June 10, 1999 and received an accession number of FERM P-17416, and it was transferred to an international deposition under the provisions of the Budapest Treaty on March 31, 2000, and received an accession number of FERM BP-7112.

Example 4

Creation of L-threonine-producing bacterium

(1) Introduction of threonine operon plasmid into *Methylophilus* bacterium

[0111] A plasmid pVIC40 (International Publication WO90/04636, Japanese Patent Application Laid-open (Kohyo) No. 3-501682/1991) containing a threonine operon derived from *E. coli* was introduced into the *Methylophilus methylotrophus* AS1 strain (NCIMB10515) by electroporation (Canadian Journal of Microbiology, 43, 197 (1997)) to obtain AS1/pVIC40 strain. As a control, pRS (Japanese Patent Application Laid-open (Kohyo) No. 3-501682/1991) having only the vector region was obtained by deleting the DNA region coding for the threonine operon from the pVIC40 plasmid, and it was introduced into the AS1 strain in the same manner as used for pVIC40 to obtain AS1/pRS strain.

(2) Production of L-threonine by *Methylophilus* bacterium containing threonine operon derived from *E. coli*

[0112] Each of the AS1/pVIC40 and AS1/pRS strains was inoculated to 121 production medium containing 20 mg/L of streptomycin, 1 g/l of L-valine and 1 g/l of L-leucine, and cultured at 37°C for 50 hours with shaking. After the culture was completed, the cells and calcium carbonate were removed by centrifugation, and L-threonine concentration in the culture supernatant was measured by an amino acid analyzer (JASCO Corporation [Nihon Bunko], high performance liquid chromatography). The results are shown in Table 5.

Table 5

Strain	Production amount of L-threonine (mg/L)
AS1/pRS	15
AS1/pVIC40	30

Example 5

Creation of branched chain amino acid-producing bacterium

[0113] The *Methylophilus methylotrophus* AS1 strain (NCIMB10515) was inoculated to 121M1 medium and cultured at 37°C for 15 hours. The obtained bacterial cells were treated with NTG in a conventional manner (NTG concentration: 100 mg/L, 37°C, 5 minutes), and spread onto 121M1 agar medium containing 0.5% of casamino acid (DIFCO). The cells were cultured at 37°C for 2 to 8 days, and allowed to form colonies. The formed colonies were picked up, and inoculated to 121M1 agar medium and 121M1 agar medium containing 0.5% of casamino acid. Strains exhibiting better growth on the latter medium compared with on the former medium were selected as casamino acid auxotrophic strains. In this way, 9 leaky casamino acid auxotrophic strains were obtained from NTG-treated 500 strains. From these casamino acid auxotrophic strains, one strain that accumulated more L-valine, L-leucine and L-isoleucine in the medium compared with its parent strain was obtained. This strain was designated as *Methylophilus methylotrophus* C138 strain.

[0114] The *Methylophilus methylotrophus* C138 strain was given a private number of AJ13609, and was deposited

at National Institute of Bioscience and Human-Technology, Agency of Industrial Science and Technology, Ministry of International Trade and Industry (postal code 305-8566, 1-3 Higashi 1-chome, Tsukuba-shi, Ibaraki-ken, Japan) on June 10, 1999 and received an accession number of FERM P-17417, and it was transferred to an international deposition under the provisions of the Budapest Treaty on March 31, 2000, and received an accession number of FERM BP-7113.

[0115] The parent strain (AS1 strain) and the C138 strain were inoculated to 121 production medium, and cultured at 37°C for 34 hours under an aerobic condition. After the culture was completed, the cells and calcium carbonate were removed from the medium by centrifugation, and concentrations of L-valine, L-leucine and L-isoleucine in the culture supernatant were measured by an amino acid analyzer (JASCO Corporation [Nihon Bunko], high performance liquid chromatography). The results are shown in Table 6.

Table 6

Strain	L-valine (mg/L)	L-leucine (mg/L)	L-isoleucine (mg/L)
AS1	7.5	5.0	2.7
C138	330	166	249

Example 6

Preparation of chromosome DNA library of *Methylophilus methylotrophus* AS1 strain(1) Preparation of chromosome DNA of *Methylophilus methylotrophus* AS1 strain

[0116] One platinum loop of the *Methylophilus methylotrophus* AS1 strain (NCIMB10515) was inoculated to 5 ml of 121M1 medium in a test tube, and cultured at 37°C overnight with shaking. The obtained culture broth was inoculated to 50 ml of 121M1 medium in a 500 ml-volume Sakaguchi flask in an amount of 1%, and cultured at 37°C overnight with shaking. Then, the cells were harvested by centrifugation, and suspended in 50 ml of TEN solution (solution containing 50 mM Tris-HCl (pH 8.0), 10 mM EDTA and 20 mM NaCl (pH 8.0)). The cells were collected by centrifugation, and suspended again in 5 ml of the TEN solution containing 5 mg/ml of lysozyme and 10 µg/ml of RNase A. The suspension was maintained at 37°C for 30 minutes, and then proteinase K and sodium laurylsulfate were added thereto to final concentrations of 10 µg/ml and 0.5% (wt/vol), respectively.

[0117] The suspension was maintained at 70°C for 2 hours, and then an equal amount of a saturated solution of phenol (phenol solution saturated with 10 mM Tris-HCl (pH 8.0)) was added and mixed. The suspension was centrifuged, and the supernatant was collected. An equal amount of phenol/chloroform solution (phenol:chloroform:isoamyl alcohol = 25:24:1) was added and mixed, and the mixture was centrifuged. The supernatant was collected, and an equal amount of chloroform solution (chloroform:isoamyl alcohol = 24:1) was added thereto to repeat the same extraction procedure. To the supernatant, a 1/10 volume of 3 M sodium acetate (pH 4.8) and 2.5-fold volume of ethanol were added to precipitate chromosome DNA. The precipitates were collected by centrifugation, washed with 70% ethanol, dried under reduced pressure, and dissolved in a suitable amount of TE solution (10 mM Tris-HCl, 1 mM EDTA (pH 8.0)).

(2) Preparation of gene library

[0118] A 50 µl portion of the chromosome DNA (1 µg/µl) obtained in the above (1), 20 µl of H buffer (500 mM Tris-HCl, 100 mM MgCl₂, 10 mM dithiothreitol, 1000 mM NaCl (pH 7.5)) and 8 units of a restriction enzyme *Sau3A*I (Takara Shuzo) were allowed to react at 37°C for 10 minutes in a total volume of 200 µl, and then 200 µl of the phenol/chloroform solution was added and mixed to stop the reaction. The reaction mixture was centrifuged, and the upper layer was collected and separated on a 0.8% agarose gel. DNA corresponding to 2 to 5 kilobase pair (henceforth abbreviated as "kbp") was collected by using Concert™ Rapid Gel Extraction System (DNA collecting kit, GIBCO BRL Co.). In this way, 50 µl of a solution of DNA with fractionated size was obtained.

[0119] On the other hand, 2.5 µg of plasmid pUC118 (Takara Shuzo), 2 µl of K buffer (200 mM Tris-HCl, 100 mM MgCl₂, 10 mM dithiothreitol, 1000 mM KCl (pH 8.5)) and 10 units of restriction enzyme *Bam*HI (Takara Shuzo) were allowed to react at 37°C for 2 hours in a total volume of 20 µl, then 20 units of calf small intestine alkaline phosphatase (Takara Shuzo) was added and mixed, and the mixture was allowed to react for further 30 minutes. The reaction mixture was mixed with an equal amount of the phenol/chloroform solution, and the mixture was centrifuged. The supernatant was collected, and an equal amount of the chloroform solution was added thereto to repeat a similar extraction procedure. To the supernatant, a 1/10 volume of 3 M sodium acetate (pH 4.8) and 2.5-fold volume of ethanol were added to precipitate DNA. The DNA was collected by centrifugation, washed with 70% ethanol, dried under reduced pressure,

and dissolved in a suitable amount of TE solution.

[0120] A *Sau3A*I digestion product of the chromosome DNA prepared as described above and a *Bam*HI digestion product of pUC118 were ligated by using a Ligation Kit ver. 2 (Takara Shuzo). To the reaction mixture, a 1/10 volume of 3 M sodium acetate (pH 4.8) and 2.5-fold volume of ethanol were added to precipitate DNA. The DNA was collected by centrifugation, washed with 70% ethanol, dried under reduced pressure, and dissolved in TE solution (Ligase solution A).

[0121] In the same manner as in the above procedure, fragments obtained by partial digestion of the chromosome DNA with a restriction enzyme *A*/I (Takara Shuzo) and a *Sma*I digestion product of plasmid pSTV29 (Takara Shuzo) were ligated (Ligase solution B).

[0122] One platinum loop of *E. coli* JM109 was inoculated to 5 ml of L medium in a test tube, and cultured at 37°C overnight with shaking. The obtained culture broth was inoculated to 50 ml of L medium in a 500 ml-volume Sakaguchi flask in an amount of 1%, cultured at 37°C until OD₆₆₀ of the culture became 0.5 to 0.6, and cooled on ice for 15 minutes. Then, the cells were harvested by centrifugation at 4°C. The cells were suspended in 50 ml of ice-cooled water and centrifuged to wash the cells. This operation was repeated once again, and the cells were suspended in 50 ml of ice-cooled 10% glycerol solution, and centrifuged to wash the cells. The cells were suspended in 10% glycerol solution of the same volume as the cells, and divided into 50 µl aliquots. To the cells in the 50 µl volume, 1 µl of Ligase solution A or Ligase solution B prepared above was added. Then, the mixture was put into a special cuvette (0.1 cm width, preliminarily ice-cooled) for an electroporation apparatus of BioRad.

[0123] The setting of the apparatus was 1.8 kV and 25 µF, and the setting of pulse controller was 200 ohms. The cuvette was mounted on the apparatus and pulses were applied thereto. Immediately after the application of pulse, 1 ml of ice-cooled SOC medium was added thereto, and the mixture was transferred into a sterilized test tube, and cultured at 37°C for 1 hour with shaking. Each cell culture broth was spread onto L agar medium containing an antibiotic (100 µg/ml of ampicillin when Ligase solution A was used, or 20 µg/ml of chloramphenicol when Ligase solution B was used), and incubated at 37°C overnight. The colonies emerged on each agar medium were scraped, inoculated to 50 ml of L medium containing respective antibiotic in a 500 ml-volume Sakaguchi flask, and cultured at 37°C for 2 hours with shaking. Plasmid DNA was extracted from each culture broth by the alkali SDS method to form Gene library solution A and Gene library solution B, respectively.

Example 7

Cloning of lysine biosynthesis gene of *Methylophilus methylotrophus* AS1 strain

(1) Cloning of gene coding for aspartokinase (AK)

[0124] *E. coli* GT3 deficient in the three genes coding for AK (*thrA*, *metLM* and *lysC*) was transformed with Gene library solution B by the same electroporation procedure as mentioned above. SOC medium containing 20 µg/ml of diaminopimelic acid was added to the transformation solution, and cultured at 37°C with shaking. Then, the culture broth was spread onto L medium containing 20 µg/ml of diaminopimelic acid and 20 µg/ml of chloramphenicol to obtain emerged colonies. This was replicated as a master plate to M9 agar medium containing 20 µg/ml of chloramphenicol, and the replicate was incubated at 37°C for 2 to 3 days. The host could not grow in M9 minimal medium that did not contain diaminopimelic acid since it did not have AK activity. In contrast, it was expected that the transformant strain that contained the gene coding for AK derived from *Methylophilus methylotrophus* could grow in M9 minimal medium because of the function of the gene.

[0125] Two transformants out of about 3000 transformants formed colonies on M9 medium. Plasmids were extracted from the colonies emerged on M9 medium and analyzed. As a result, the presence of an inserted fragment on the plasmids was confirmed. The plasmids were designated as pMMASK-1 and pMMASK-2, respectively. By using these plasmids, *E. coli* GT3 was transformed again. The obtained transformants could grow on M9 minimal medium. Further, the transformant which contained each of these plasmids was cultured overnight in L medium containing 20 µg/ml of chloramphenicol, and the cells were collected by centrifugation of the culture broth. Cell-free extracts were prepared by sonicating the cells, and AK activity was measured according to the method of Miyajima et al. (Journal of Biochemistry (Tokyo), vol. 63, 139-148 (1968)) (Fig. 3: pMMASK-1, pMMASK-2). In addition, a GT3 strain harboring the vector pSTV29 was similarly cultured in L medium containing 20 µg/ml of diaminopimelic acid and 20 µg/ml of chloramphenicol, and AK activity was measured (Fig. 3: Vector). As a result, increase in AK activity was observed in two of the clones containing the inserted fragments compared with the transformant harboring only the vector. Therefore, it was confirmed that the gene that could be cloned on pSTV29 was a gene coding for AK derived from *Methylophilus methylotrophus*. This gene was designated as *ask*.

[0126] The DNA nucleotide sequence of the *ask* gene was determined by the dideoxy method. It was found that pMMASK-1 and pMMASK-2 contained a common fragment. The nucleotide sequence of the DNA fragment containing

the *ask* gene derived from *Methylophilus methylotrophus* is shown in SEQ ID NO: 5. An amino acid sequence that can be encoded by the nucleotide sequence is shown in SEQ ID NOS: 5 and 6.

(2) Cloning of gene coding for aspartic acid semialdehyde dehydrogenase (ASD)

[0127] *E. coli* Hfr3000 U482 (CGSC 5081 strain) deficient in the *asd* gene was transformed by electroporation using Gene library solution B in the same manner as described above. To the transformation solution, SOC medium containing 20 µg/ml of diaminopimelic acid was added and the mixture was cultured at 37°C with shaking. The cells were harvested by centrifugation. The cells were washed by suspending them in L medium and centrifuging the suspension. The same washing operation was repeated once again, and the cells were suspended in L medium. Then, the suspension was spread onto L agar medium containing 20 µg/ml of chloramphenicol, and incubated overnight at 37°C. The host showed extremely slow growth in L medium not containing diaminopimelic acid since it was deficient in the *asd* gene. In contrast, it was expected that normal growth would be observed for a transformant strain which contained the gene coding for ASD derived from *Methylophilus methylotrophus* even in L medium because of the function of the gene. Further, the host *E. coli* could not grow in M9 minimal medium, but a transformant strain that contained the gene coding for ASD derived from *Methylophilus methylotrophus* was expected to be able to grow in M9 minimal medium because of the function of the gene. Therefore, colonies of transformants that normally grew on L medium were picked up, streaked and cultured on M9 agar medium. As a result, growth was observed. Thus, it was confirmed that the gene coding for ASD functioned in these transformant strains as expected.

[0128] Plasmids were extracted from the three transformant strains emerged on M9 medium, and the presence of an inserted fragment in the plasmids was confirmed. The plasmids were designated as pMMASD-1, pMMASD-2 and pMMASD-3, respectively. When the *E. coli* Hfr3000 U482 was transformed again by using these plasmids, each transformant grew in M9 minimal medium. Further, each transformant was cultured overnight in L medium containing 20 µg/ml of chloramphenicol, and the cells were collected by centrifugation of the culture broth. The cells were sonicated to prepare a crude enzyme solution, and ASD activity was measured according to the method of Boy et al. (Journal of Bacteriology, vol. 112 (1), 84-92 (1972)) (Fig. 4: pMMASD-1, pMMASD-2, pMMASD-3). In addition, the host harboring the vector was similarly cultured in L medium containing 20 µg/ml of diaminopimelic acid and 20 µg/ml of chloramphenicol, and ASD activity was measured as a control experiment (Fig. 4: Vector). As a result, the enzymatic activity could not be detected for the transformant harboring only the vector, whereas the ASD activity could be detected in three of the clones having an insert fragment. Therefore, it was confirmed that the obtained gene was a gene coding for ASD derived from *Methylophilus methylotrophus* (designated as *asd*).

[0129] The DNA nucleotide sequence of the *asd* gene was determined by the dideoxy method. It was found that all of the three obtained clones contained a common fragment. The nucleotide sequence of the DNA fragment containing the *asd* gene derived from *Methylophilus methylotrophus* is shown in SEQ ID NO: 7. An amino acid sequence that can be encoded by the nucleotide sequence is shown in SEQ ID NOS: 7 and 8.

(3) Cloning of gene coding for dihydrodipicolinate synthase (DDPS)

[0130] *E. coli* AT997 (CGSC 4547 strain) deficient in the *dapA* gene was transformed by the same electroporation procedure using Gene library solution A. To the transformation solution, SOC medium containing 20 µg/ml of diaminopimelic acid was added, and the mixture was cultured at 37°C with shaking. Then, the culture broth was spread onto L medium containing 20 µg/ml of diaminopimelic acid and 100 µg/ml of ampicillin to obtain emerged colonies. This was replicated as a master plate to M9 minimal agar medium containing 100 µg/ml of ampicillin, and the replicate was incubated at 37°C for 2 to 3 days. The host could not grow in M9 minimal medium that did not contain diaminopimelic acid since it was deficient in *dapA* gene. In contrast, it was expected that a transformant strain that contained the gene coding for DDPS derived from *Methylophilus methylotrophus* could grow in M9 minimal medium because of the function of that gene.

[0131] Plasmids were extracted from the colonies of two strains emerged on M9 medium, and analyzed. As a result, the presence of an inserted fragment in the plasmids was confirmed. The plasmids were designated as pMMDAPA-1 and pMMDAP-2, respectively. When *E. coli* AT997 was transformed again by using these plasmids, each transformant was grown in M9 minimal medium. Further, each transformant containing each plasmid was cultured overnight in L medium containing 100 µg/ml of ampicillin, and the cells were collected by centrifugation of the culture broth. The cells were sonicated to prepare a cell extract, and DDPS activity was measured according to the method of Yugari et al. (Journal of Biological Chemistry, vol. 240, and p. 4710 (1965)) (Fig. 5: pMMDAPA-1, pMMDAPA-2). In addition, the host harboring the vector was similarly cultured in L medium containing 20 µg/ml of diaminopimelic acid and 100 µg/ml of ampicillin, and DDPS activity was measured as a control experiment (Fig. 5: Vector). As a result, the enzymatic activity could not be detected for the transformant harboring only the vector, whereas the DDPS activity could be detected in each of the transformants harboring the plasmids having the insert fragment. Therefore, it was confirmed that the

obtained gene was a gene coding for DDPS derived from *Methylophilus methylotrophus* (designated as *dapA*).
 [0132] The DNA nucleotide sequence of the *dapA* gene was determined by the dideoxy method. It was found that two of the inserted fragments contained a common fragment. The nucleotide sequence of the DNA fragment containing the *dapA* gene derived from *Methylophilus methylotrophus* is shown in SEQ ID NO: 9. An amino acid sequence that can be encoded by the nucleotide sequence is shown in SEQ ID NOS: 9 and 10.

(4) Cloning of gene coding for dihydrodipicolinate reductase (DDPR)

[0133] *E. coli* AT999 (CGSC 4549 strain) deficient in the *dapB* gene was transformed by the same electroporation procedure as described above using Gene library solution A. To the transformation solution, SOC medium containing 20 µg/ml of diaminopimelic acid was added, and the mixture was cultured at 37°C with shaking. Then, the cells were harvested by centrifugation. The cells were washed by suspending them in L medium and centrifuging the suspension. The same washing operation was repeated once again, and the cells were suspended in L medium. Then, the suspension was spread onto L agar medium containing 100 µg/ml of ampicillin, and incubated overnight at 37°C. The host showed extremely slow growth in L medium not containing diaminopimelic acid since it was deficient in the *dapB* gene. In contrast, it was expected that normal growth could be observed for a transformant strain that contained the gene coding for DDPR derived from *Methylophilus methylotrophus* even in L medium because of the function of the gene. Further, the host *E. coli* could not grow in M9 minimal medium, but it was expected that a transformant strain which contained the gene coding for DDPR derived from *Methylophilus methylotrophus* could grow in M9 minimal medium because of the function of the gene.

[0134] Therefore, a colony of transformant that normally grew on L medium was streaked and cultured on M9 agar medium. Then, growth was also observed on M9 medium. Thus, it was confirmed that the gene coding for DDPR functioned in the transformant strain. A plasmid was extracted from the colony emerged on M9 medium, and the presence of an inserted fragment in the plasmid was confirmed. When *E. coli* AT999 was transformed again by using the plasmid (pMMDAPB), the transformant grew in M9 minimal medium. Further, the transformant containing the plasmid was cultured overnight in L medium, and the cells were collected by centrifugation of the culture broth. The cells were sonicated to prepare a cell extract, and DDPR activity was measured according to the method of Tamir et al. (Journal of Biological Chemistry, vol. 249, p.3034 (1974)) (Fig. 6: pMMDAPB). In addition, the host harboring the vector was similarly cultured in L medium containing 20 µg/ml diaminopimelic acid and 100 µg/ml of ampicillin, and DDPR activity was measured as a control experiment (Fig. 6: Vector). As a result, the enzymatic activity could not be detected for the transformant harboring only the vector, whereas the DDPR activity could be detected for the transformant harboring pMMDAPB. Therefore, it was confirmed that the obtained gene was a gene coding for DDPR derived from *Methylophilus methylotrophus* (designated as *dapB*).

[0135] The DNA nucleotide sequence of the *dapB* gene was determined by the dideoxy method. The nucleotide sequence of the DNA fragment containing the *dapB* gene derived from *Methylophilus methylotrophus* is shown in SEQ ID NO: 11. An amino acid sequence that can be encoded by the nucleotide sequence is shown in SEQ ID NOS: 11 and 12.

(5) Cloning of gene coding for diaminopimelate decarboxylase (DPDC)

[0136] *E. coli* AT2453 (CGSC 4505 strain) deficient in the *lysA* gene was transformed by the same electroporation procedure as described above using Gene library solution A. The transformation solution, SOC medium was added, and the mixture was cultured at 37°C with shaking. The cells were harvested by centrifugation. The cells were washed by suspending them in 5 ml of sterilized water and centrifuging the suspension. The same washing operation was repeated once again, and the cells were suspended in 500 µl of sterilized water. Then, the suspension was spread onto M9 minimal agar medium containing 20 µg/ml of chloramphenicol, and incubated at 37°C for 2 to 3 days. The host could not grow in M9 minimal medium not containing lysine since it was deficient in the *lysA* gene. In contrast, it was expected that a transformant strain that contained the gene coding for DPDC derived from *Methylophilus methylotrophus* could grow in M9 minimal medium because of the function of the gene.

[0137] Therefore, plasmids were extracted from the three transformant strains emerged on M9 medium, and analyzed. As a result, the presence of an inserted fragment in the plasmids was confirmed. The plasmids were designated as pMMLYSA-1, pMMLYSA-2 and pMMLYSA-3, respectively. When *E. coli* AT2453 was transformed again by using each of these plasmids, each transformant grew in M9 minimal medium. Further, each transformant containing each plasmid was cultured overnight in L medium containing 20 µg/ml of chloramphenicol, and the cells were collected by centrifugation of the culture broth. The cells were sonicated to prepare a cell extract, and DPDC activity was measured according to the method of Cremer et al. (Journal of General Microbiology, vol. 134, 3221-3229 (1988)) (Fig. 7: pMMLYSA-1, pMMLYSA-2, pMMLYSA-3). In addition, the host harboring the vector was similarly cultured in L medium containing 20 µg/ml of chloramphenicol, and DPDC activity was measured as a control experiment (Fig. 7: Vector). As a

result, the enzymatic activity could not be detected for the transformant harboring only the vector, whereas the DPDC activity could be detected in three of the clones having an insert fragment. Therefore, it was confirmed that the obtained gene was a gene coding for DPDC derived from *Methylophilus methylotrophus* (designated as *lysA*).

[0138] The DNA nucleotide sequence of the *lysA* gene was determined by the dideoxy method. It was found that all of the three inserted fragments contained a common DNA fragment. The nucleotide sequence of the DNA fragment containing the *lysA* gene derived from *Methylophilus methylotrophus* is shown in SEQ ID NO: 13. An amino acid sequence that can be encoded by the nucleotide sequence is shown in SEQ ID NOS: 13 and 14.

Industrial Applicability

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[0139] According to the present invention, there are provided a *Methylophilus* bacterium having L-amino acid-producing ability, a method for producing an L-amino acid using the *Methylophilus* bacterium, and *Methylophilus* bacterial cells with increased content of an L-amino acid. By the method of the present invention, it is enabled to produce an L-amino acid using methanol as a raw material. Moreover, novel L-lysine biosynthesis enzyme genes derived from *Methylophilus* bacteria are provided by the present invention.

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SEQUENCE LISTING

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40	tgt cag att tat acc gat gtc gat ggc gtt tac acc acc gat ccg cgt				1061
	Cys Gln Ile Tyr Thr Asp Val Asp Gly Val Tyr Thr Thr Asp Pro Arg				
	170	175	180		
	gtg gtg cct gag gca cgc cgc ttg gat aaa att acc ttt gaa gaa atg				1109
45	Val Val Pro Glu Ala Arg Arg Leu Asp Lys Ile Thr Phe Glu Glu Met				
	185	190	195	200	
	ttg gaa ctg gct tca cag ggc tcc aaa gta ttg caa att cgc tgc gtt				1157
	Leu Glu Leu Ala Ser Gln Gly Ser Lys Val Leu Gln Ile Arg Ser Val				
50	205	210	215		
	gag ttt gcc ggt aaa tac aaa gtc aaa tta cgt gtg ctg tcc agc ttc				1205
	Glu Phe Ala Gly Lys Tyr Lys Val Lys Leu Arg Val Leu Ser Ser Phe				
	220	225	230		
55	gaa gag gag ggc gac ggt aca ctg atc aca ttc gaa gaa aat gag gaa				1253

Glu Glu Glu Gly Asp Gly Thr Leu Ile Thr Phe Glu Glu Asn Glu Glu
 235 240 245
 5 aac atg gaa gaa cca att atc tcc ggc atc gcc ttt aac cgc gat gag 1301
 Asn Met Glu Glu Pro Ile Ile Ser Gly Ile Ala Phe Asn Arg Asp Glu
 250 255 260
 10 gcg aaa att acc gtg acg ggc gtg ccc gac aaa cca gga att gcc tat 1349
 Ala Lys Ile Thr Val Thr Gly Val Pro Asp Lys Pro Gly Ile Ala Tyr
 265 270 275 280
 15 cag att ttg ggc ccg gtg gca gac gcc aat att gat gtg gat atg att 1397
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 285 290 295
 20 atc cag aac gtc ggt gcg gat ggt acg act gac ttc acc ttt acc gta 1445
 Ile Gln Asn Val Gly Ala Asp Gly Thr Thr Asp Phe Thr Phe Thr Val
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 cat aaa aat gag atg aac aaa gcc ctg agc att ctt aga gat aaa gtg 1493
 His Lys Asn Glu Met Asn Lys Ala Leu Ser Ile Leu Arg Asp Lys Val
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 Gln Gly His Ile Gln Ala Arg Glu Ile Ser Gly Asp Asp Lys Ile Ala
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 30 aaa gtc tct gtg gtt ggg gtg ggt atg cgc tca cat gta ggg atc gcc 1589
 Lys Val Ser Val Val Gly Val Gly Met Arg Ser His Val Gly Ile Ala
 345 350 355 360
 35 agc cag atg ttc cgt acg ctg gcc gaa gaa ggg atc aat att caa atg 1637
 Ser Gln Met Phe Arg Thr Leu Ala Glu Glu Gly Ile Asn Ile Gln Met
 365 370 375
 40 atc tca acc agc gaa att aaa att gca gtc gtg atc gaa gag aag tac 1685
 Ile Ser Thr Ser Glu Ile Lys Ile Ala Val Val Ile Glu Glu Lys Tyr
 380 385 390
 45 atg gaa ctg gct gta cgc gtg ttg cat aaa gca ttc ggc ctc gaa aac 1733
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 Ala
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Arg Leu Ile Ser Leu Ala Lys Glu Ile Met Gln Asp Pro Asp Pro Arg
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Glu Leu Asp Val Met Val Ser Thr Gly Glu Gln Val Thr Ile Gly Met
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Thr Ala Leu Ala Leu Met Glu Leu Gly Ile Lys Ala Lys Ser Tyr Thr
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Gly Thr Gln Val Lys Ile Leu Thr Asp Asp Ala Phe Thr Lys Ala Arg
 100 105 110

Ile Leu Asp Ile Asp Glu His Asn Leu Lys Lys Asp Leu Asp Asp Gly
 115 120 125

Tyr Val Cys Val Val Ala Gly Phe Gln Gly Val Asp Ala Asn Gly Asn
 130 135 140

Ile Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Gly Val Ala Leu
 145 150 155 160

Ala Ala Ala Leu Lys Ala Asp Glu Cys Gln Ile Tyr Thr Asp Val Asp
 165 170 175

Gly Val Tyr Thr Thr Asp Pro Arg Val Val Pro Glu Ala Arg Arg Leu
 180 185 190

Asp Lys Ile Thr Phe Glu Glu Met Leu Glu Leu Ala Ser Gln Gly Ser
 195 200 205

Lys Val Leu Gln Ile Arg Ser Val Glu Phe Ala Gly Lys Tyr Lys Val
 210 215 220

Lys Leu Arg Val Leu Ser Ser Phe Glu Glu Glu Gly Asp Gly Thr Leu
 225 230 235 240

Ile Thr Phe Glu Glu Asn Glu Glu Asn Met Glu Glu Pro Ile Ile Ser

245 250 255
 Gly Ile Ala Phe Asn Arg Asp Glu Ala Lys Ile Thr Val Thr Gly Val
 260 265 270
 5 Pro Asp Lys Pro Gly Ile Ala Tyr Gln Ile Leu Gly Pro Val Ala Asp
 275 280 285
 Ala Asn Ile Asp Val Asp Met Ile Ile Gln Asn Val Gly Ala Asp Gly
 10 290 295 300
 Thr Thr Asp Phe Thr Phe Thr Val His Lys Asn Glu Met Asn Lys Ala
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 15 Leu Ser Ile Leu Arg Asp Lys Val Gln Gly His Ile Gln Ala Arg Glu
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 340 345 350
 20 Met Arg Ser His Val Gly Ile Ala Ser Gln Met Phe Arg Thr Leu Ala
 355 360 365
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Met Leu Lys Val Gly Phe

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gta ggc tgg cgt ggc atg gtt gga tcc gtg cta atg cag cgc atg atg 163

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Val Gly Trp Arg Gly Met Val Gly Ser Val Leu Met Gln Arg Met Met

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	Gln Glu Asn Asp Phe Ala Asp Ile Glu Pro Gln Phe Phe Thr Thr Ser			
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	Gln Thr Gly Gly Ala Ala Pro Lys Val Gly Lys Asp Thr Pro Ala Leu			
	40	45	50	
15	aaa gat gcc aag gat att gat gct ttg cgc cag atg gat gtg att gtg			307
	Lys Asp Ala Lys Asp Ile Asp Ala Leu Arg Gln Met Asp Val Ile Val			
	55	60	65	70
20	acc tgc cag ggt ggc gat tac acg agt gac gtc ttc cca caa ttg cgc			355
	Thr Cys Gln Gly Gly Asp Tyr Thr Ser Asp Val Phe Pro Gln Leu Arg			
	75	80	85	
25	gca acc ggc tgg agc ggc cac tgg att gac gcg gcc tct acc tta cgc			403
	Ala Thr Gly Trp Ser Gly His Trp Ile Asp Ala Ala Ser Thr Leu Arg			
	90	95	100	
30	atg gaa aaa gac tcc gtg atc att tta gac ccg gtg aac atg cat gtg			451
	Met Glu Lys Asp Ser Val Ile Ile Leu Asp Pro Val Asn Met His Val			
	105	110	115	
35	att aaa gat gca ttg tcc aat ggc ggc aaa aac tgg atc ggc ggc aac			499
	Ile Lys Asp Ala Leu Ser Asn Gly Gly Lys Asn Trp Ile Gly Gly Asn			
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	Cys Thr Val Ser Leu Met Leu Met Ala Leu Asn Gly Leu Phe Lys Ala			
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45	gac ctg gtc gag tgg gcc act tcc atg acc tac cag gcg gct tca ggc			595
	Asp Leu Val Glu Trp Ala Thr Ser Met Thr Tyr Gln Ala Ala Ser Gly			
	155	160	165	
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	Ala Gly Ala Gln Asn Met Arg Glu Leu Ile Ser Gln Met Gly Val Val			
	170	175	180	
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	Asn Ala Ser Val Ala Asp Leu Leu Ala Asp Pro Ala Ser Ala Ile Leu			
	185	190	195	
60	cag atc gat aaa aca gtg gcg gat acc atc cgt agc gaa gag ttg cct			739
	Gln Ile Asp Lys Thr Val Ala Asp Thr Ile Arg Ser Glu Glu Leu Pro			
	200	205	210	
65	aaa tct aac ttt ggt gtg cca ttg gcg ggc agt ctg atc cca tgg atc			787

Lys Ser Asn Phe Gly Val Pro Leu Ala Gly Ser Leu Ile Pro Trp Ile
 215 220 225 230
 5 gac aag gac tta ggg aat ggt caa agt aaa gaa gaa tgg aag ggc ggc 835
 Asp Lys Asp Leu Gly Asn Gly Gln Ser Lys Glu Glu Trp Lys Gly Gly
 235 240 245
 10 gta nag acc aat aag att tta ggt cgt gaa gcg aac ccg att gtg att 883
 Val Xaa Thr Asn Lys Ile Leu Gly Arg Glu Ala Asn Pro Ile Val Ile
 250 255 260
 15 gac ggt ttg tgt gta cgt atc ggc gcc atg cgt tgc cat tca caa gcg 931
 Asp Gly Leu Cys Val Arg Ile Gly Ala Met Arg Cys His Ser Gln Ala
 265 270 275
 20 ttg act atc aag ctg cgc aag gat gtg ccg ctg gat gaa atc aat cag 979
 Leu Thr Ile Lys Leu Arg Lys Asp Val Pro Leu Asp Glu Ile Asn Gln
 280 285 290
 atg ctg gct gaa gcg aac gac tgg gct aaa gtc att ccc aat gag cgt 1027
 Met Leu Ala Glu Ala Asn Asp Trp Ala Lys Val Ile Pro Asn Glu Arg
 25 295 300 305 310
 gag gtc agt atg cgg gaa ctc acc ccg gca gcg att acc ggc agt ctg 1075
 Glu Val Ser Met Arg Glu Leu Thr Pro Ala Ala Ile Thr Gly Ser Leu
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 30 gcg acg cca gta ggg cgt ttg cgc aaa ctg gcg atg ggt ggt gaa tac 1123
 Ala Thr Pro Val Gly Arg Leu Arg Lys Leu Ala Met Gly Gly Glu Tyr
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 35 ttg tgg gca ttt acc gta ggt gac cag ttg tta tgg ggc gct gcc gaa 1171
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 40 cct ttg cgc aga atg ttg agg att ctg gtc gaa tct taagtaattg 1217
 Pro Leu Arg Arg Met Leu Arg Ile Leu Val Glu Ser
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 45 tttaagtagc agcccgtaaa gctatgattt atcaataaaa tcatggtctt ttcgggcttt 1277
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 Lys Asp Thr Pro Ala Leu Lys Asp Ala Lys Asp Ile Asp Ala Leu Arg
 50 55 60
 15 Gln Met Asp Val Ile Val Thr Cys Gln Gly Gly Asp Tyr Thr Ser Asp
 65 70 75 80
 Val Phe Pro Gln Leu Arg Ala Thr Gly Trp Ser Gly His Trp Ile Asp
 85 90 95
 20 Ala Ala Ser Thr Leu Arg Met Glu Lys Asp Ser Val Ile Ile Leu Asp
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 25 Pro Val Asn Met His Val Ile Lys Asp Ala Leu Ser Asn Gly Gly Lys
 115 120 125
 Asn Trp Ile Gly Gly Asn Cys Thr Val Ser Leu Met Leu Met Ala Leu
 130 135 140
 30 Asn Gly Leu Phe Lys Ala Asp Leu Val Glu Trp Ala Thr Ser Met Thr
 145 150 155 160
 Tyr Gln Ala Ala Ser Gly Ala Gly Ala Gln Asn Met Arg Glu Leu Ile
 165 170 175
 35 Ser Gln Met Gly Val Val Asn Ala Ser Val Ala Asp Leu Leu Ala Asp
 180 185 190
 Pro Ala Ser Ala Ile Leu Gln Ile Asp Lys Thr Val Ala Asp Thr Ile
 195 200 205
 40 Arg Ser Glu Glu Leu Pro Lys Ser Asn Phe Gly Val Pro Leu Ala Gly
 210 215 220
 45 Ser Leu Ile Pro Trp Ile Asp Lys Asp Leu Gly Asn Gly Gln Ser Lys
 225 230 235 240
 Glu Glu Trp Lys Gly Gly Val Xaa Thr Asn Lys Ile Leu Gly Arg Glu
 245 250 255
 50 Ala Asn Pro Ile Val Ile Asp Gly Leu Cys Val Arg Ile Gly Ala Met
 260 265 270
 Arg Cys His Ser Gln Ala Leu Thr Ile Lys Leu Arg Lys Asp Val Pro
 275 280 285

Leu Asp Glu Ile Asn Gln Met Leu Ala Glu Ala Asn Asp Trp Ala Lys
 290 295 300
 5 Val Ile Pro Asn Glu Arg Glu Val Ser Met Arg Glu Leu Thr Pro Ala
 305 310 315 320
 Ala Ile Thr Gly Ser Leu Ala Thr Pro Val Gly Arg Leu Arg Lys Leu
 325 330 335
 10 Ala Met Gly Gly Glu Tyr Leu Ser Ala Phe Thr Val Gly Asp Gln Leu
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	Thr Pro Met Phe Glu Asp Gly Arg Leu Asp Leu Asp Ala Leu Lys Lys	
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	Gly Thr Thr Gly Glu Ser Pro Thr Val Asp Val Asp Glu His Cys Leu	
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	Ala Glu Ala Val Asp Ile Pro Gln Ile Leu Tyr Asn Val Pro Gly Arg	
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Asp Phe His Val Glu Ala Gly Thr Asp Gly Ile Val Ile Val Gly Thr
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Thr Gly Glu Ser Pro Thr Val Asp Val Asp Glu His Cys Leu Leu Ile
 50 55 60

Lys Thr Thr Ile Glu His Val Ala Lys Arg Val Pro Val Ile Ala Gly
 65 70 75 80

Thr Gly Ala Asn Ser Thr Ala Glu Ala Ile Glu Leu Thr Ala Lys Ala
 85 90 95

Lys Ala Leu Gly Ala Asp Ala Cys Leu Leu Val Ala Pro Tyr Tyr Asn
 100 105 110

Lys Pro Ser Gln Glu Gly Leu Tyr Gln His Phe Lys Ala Val Ala Glu
 115 120 125

Ala Val Asp Ile Pro Gln Ile Leu Tyr Asn Val Pro Gly Arg Thr Gly
 130 135 140

Cys Asp Leu Ser Asn Asp Thr Val Leu Arg Leu Ala Gln Ile Arg Asn
 145 150 155 160

Ile Val Gly Ile Lys Asp Ala Thr Gly Gly Ile Glu Arg Gly Thr Asp
 165 170 175

Leu Leu Leu Arg Ala Pro Ala Asp Phe Ala Ile Tyr Ser Gly Asp Asp
 180 185 190

Ala Thr Ala Leu Ala Leu Met Leu Leu Gly Gly Lys Gly Val Ile Ser
 195 200 205

Val Thr Ala Asn Val Ala Pro Lys Leu Met His Glu Met Cys Glu His
 210 215 220

Ala Leu Asn Gly Asn Leu Ala Ala Lys Ala Ala Asn Ala Lys Leu
 225 230 235 240
 5 Phe Ala Leu His Gln Lys Leu Phe Val Glu Ala Asn Pro Ile Pro Val
 245 250 255
 Lys Trp Val Leu Gln Gln Met Gly Met Ile Ala Thr Gly Ile Arg Leu
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<213> *Methylophilus methylotrophus*

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<222> (2080)..(2883)

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35 40 45

25 Phe Gly Lys Val Ser Gly Val Lys Ile Thr Ala Asp Ile His Ala Ala

50 55 60

Leu Val Gly Ala Asp Val Leu Val Asp Phe Thr Arg Pro Glu Ala Ser

30 65 70 75 80

Met Gln Tyr Leu Gln Ala Cys Gln Gln Ala Asn Val Lys Leu Val Ile

85 90 95

35 Gly Thr Thr Gly Phe Ser Glu Ala Glu Lys Ala Ser Ile Glu Ala Ala

100 105 110

Ser Lys Asn Ile Gly Ile Val Phe Ala Pro Asn Met Ser Val Gly Val

115 120 125

40 Thr Leu Leu Ile Asn Leu Val Glu Gln Ala Ala Arg Val Leu Asn Glu

130 135 140

Gly Tyr Asp Ile Glu Val Val Glu Met His His Arg His Lys Val Asp

45 145 150 155 160

Ala Pro Ser Gly Thr Ala Leu Arg Leu Gly Glu Ala Ala Ala Lys Gly

165 170 175

Ile Asp Lys Ala Leu Lys Asp Cys Ala Val Tyr Ala Arg Glu Gly Val

180 185 190

50 Thr Gly Glu Arg Glu Ala Gly Thr Ile Gly Phe Ala Thr Leu Arg Gly

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55

30 Claims

1. A *Methylophilus* bacterium having L-amino acid-producing ability.
2. The *Methylophilus* bacterium according to claim 1, wherein the L-amino acid is L-lysine, L-valine, L-leucine, L-isoleucine or L-threonine.
3. The *Methylophilus* bacterium according to claim 1, which shows resistance to an L-amino acid analogue or L-amino acid auxotrophy.
4. The *Methylophilus* bacterium according to claim 1, wherein L-amino acid biosynthetic enzyme activity is enhanced.
5. The *Methylophilus* bacterium according to claim 1, wherein dihydrodipicolinate synthase activity and aspartokinase activity are enhanced, and the bacterium has L-lysine-producing ability.
6. The *Methylophilus* bacterium according to claim 1, wherein dihydrodipicolinate synthase activity is enhanced, and the bacterium has L-lysine-producing ability.
7. The *Methylophilus* bacterium according to claim 1, wherein aspartokinase activity is enhanced, and the bacterium has L-lysine-producing ability.
8. The *Methylophilus* bacterium according to any one of claims 5 to 7, wherein an activity or activities of one, two or three of enzymes selected from aspartic acid semialdehyde dehydrogenase, dihydrodipicolinate reductase and diaminopimelate decarboxylase is/are enhanced.
9. The *Methylophilus* bacterium according to claim 5, wherein the dihydrodipicolinate synthase activity and the aspartokinase activity are enhanced by transformation through introduction into cells, of a DNA coding for dihydrodipicolinate synthase that does not suffer feedback inhibition by L-lysine and a DNA coding for aspartokinase that does not suffer feedback inhibition by L-lysine.

10. The *Methylophilus* bacterium according to claim 1, wherein activities of aspartokinase, homoserine dehydrogenase, homoserine kinase and threonine synthase are enhanced, and the bacterium has L-threonine-producing ability.
- 5 11. The bacterium according to any one of claims 1 to 10, wherein the *Methylophilus* bacterium is *Methylophilus methylotrophus*.
12. A method for producing an L-amino acid, which comprises culturing a *Methylophilus* bacterium as defined in any one of claim 1 to 11 in a medium to produce and accumulate an L-amino acid in culture and collecting the L-amino
10 acid from the culture.
13. The method according to claim 12, wherein the medium contains methanol as a main carbon source.
14. A method for producing bacterial cells of a *Methylophilus* bacterium with an increased content of an L-amino acid, which comprises culturing a *Methylophilus* bacterium as defined in any one of claim 1 to 11 in a medium to produce
15 and accumulate an L-amino acid in bacterial cells of the bacterium.
15. The method for producing bacterial cells of the *Methylophilus* bacterium according to claim 14, wherein the L-amino acid is L-lysine, L-valine, L-leucine, L-isoleucine or L-threonine.
20
16. A DNA which codes for a protein defined in the following (A) or (B):
(A) a protein which has the amino acid sequence of SEQ ID NO: 6, or
25 (B) a protein which has an amino acid sequences of SEQ ID NO: 6 including substitution, deletion, insertion, addition or inversion of one or several amino acids, and has aspartokinase activity.
17. The DNA according to claim 16, which is a DNA defined in the following (a) or (b):
30 (a) a DNA which has a nucleotide sequence comprising the nucleotide sequence of the nucleotide numbers 510 to 1736 of SEQ ID NO: 5; or
(b) a DNA which is hybridizable with a probe having the nucleotide sequence of the nucleotide numbers 510 to 1736 of SEQ ID NO: 5 or a part thereof under a stringent condition, and codes for a protein having aspartokinase activity.
- 35 18. A DNA which codes for a protein defined in the following (C) or (D):
(C) a protein which has the amino acid sequence of SEQ ID NO: 8, or
(D) a protein which has an amino acid sequences of SEQ ID NO: 8 including substitution, deletion, insertion,
40 addition or inversion of one or several amino acids, and has aspartic acid semialdehyde dehydrogenase activity.
19. The DNA according to claim 18, which is a DNA defined in the following (c) or (d):
45 (c) a DNA which has a nucleotide sequence comprising the nucleotide sequence of the nucleotide numbers 98 to 1207 of SEQ ID NO: 7; or
(d) a DNA which is hybridizable with a probe having the nucleotide sequence of the nucleotide numbers 98 to 1207 of SEQ ID NO: 7 or a part thereof under a stringent condition, and codes for a protein having aspartic acid semialdehyde dehydrogenase activity.
- 50 20. A DNA which codes for a protein defined in the following (E) or (F):
(E) a protein which has the amino acid sequence of SEQ ID NO: 10, or
(F) a protein which has an amino acid sequences of SEQ ID NO: 10 including substitution, deletion, insertion,
55 addition or inversion of one or several amino acids, and has dihydrodipicolinate synthase activity.
21. The DNA according to claim 20, which is a DNA defined in the following (e) or (f):
(e) a DNA which has a nucleotide sequence comprising the nucleotide sequence of the nucleotide numbers

1268 to 2155 of SEQ ID NO: 9; or

(f) a DNA which is hybridizable with a probe having the nucleotide sequence of the nucleotide numbers 1268 to 2155 of SEQ ID NO: 9 or a part thereof under a stringent condition, and codes for a protein having dihydrodipicolinate synthase activity.

5

22. A DNA which codes for a protein defined in the following (G) or (H):

(G) a protein which has the amino acid sequence of SEQ ID NO: 12, or

10

(H) a protein which has an amino acid sequences of SEQ ID NO: 12 including substitution, deletion, insertion, addition or inversion of one or several amino acids, and has dihydrodipicolinate reductase activity.

23. The DNA according to claim 22, which is a DNA defined in the following (g) or (h):

15

(g) a DNA which has a nucleotide sequence comprising the nucleotide sequence of the nucleotide numbers 2080 to 2883 of SEQ ID NO: 11; or

(h) a DNA which is hybridizable with a probe having the nucleotide sequence of the nucleotide numbers 2080 to 2883 of SEQ ID NO: 11 or a part thereof under a stringent condition, and codes for a protein having dihydrodipicolinate reductase activity.

20

24. A DNA which codes for a protein defined in the following (I) or (J):

(I) a protein which has the amino acid sequence of SEQ ID NO: 14, or

(J) a protein which has an amino acid sequences of SEQ ID NO: 14 including substitution, deletion, insertion, addition or inversion of one or several amino acids, and has diaminopimelate decarboxylase activity.

25

25. The DNA according to claim 24, which is a DNA defined in the following (i) or (j):

(i) a DNA which has a nucleotide sequence comprising the nucleotide sequence of the nucleotide numbers 751 to 1995 of SEQ ID NO: 13; or

30

(j) a DNA which is hybridizable with a probe having the nucleotide sequence of the nucleotide numbers 751 to 1995 of SEQ ID NO: 13 or a part thereof under a stringent condition, and codes for a protein having diaminopimelate decarboxylase activity.

35

40

45

50

55

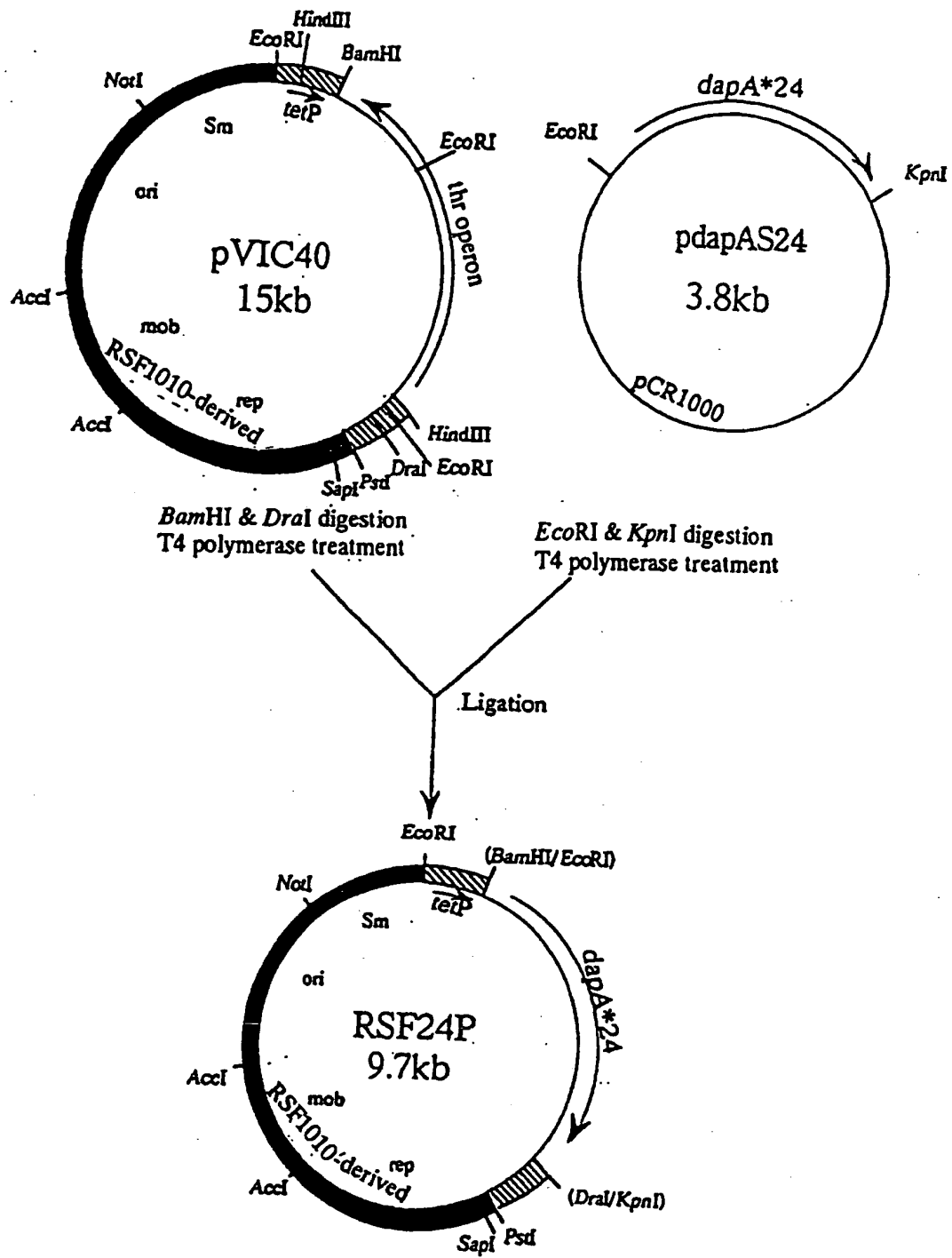


FIG. 1

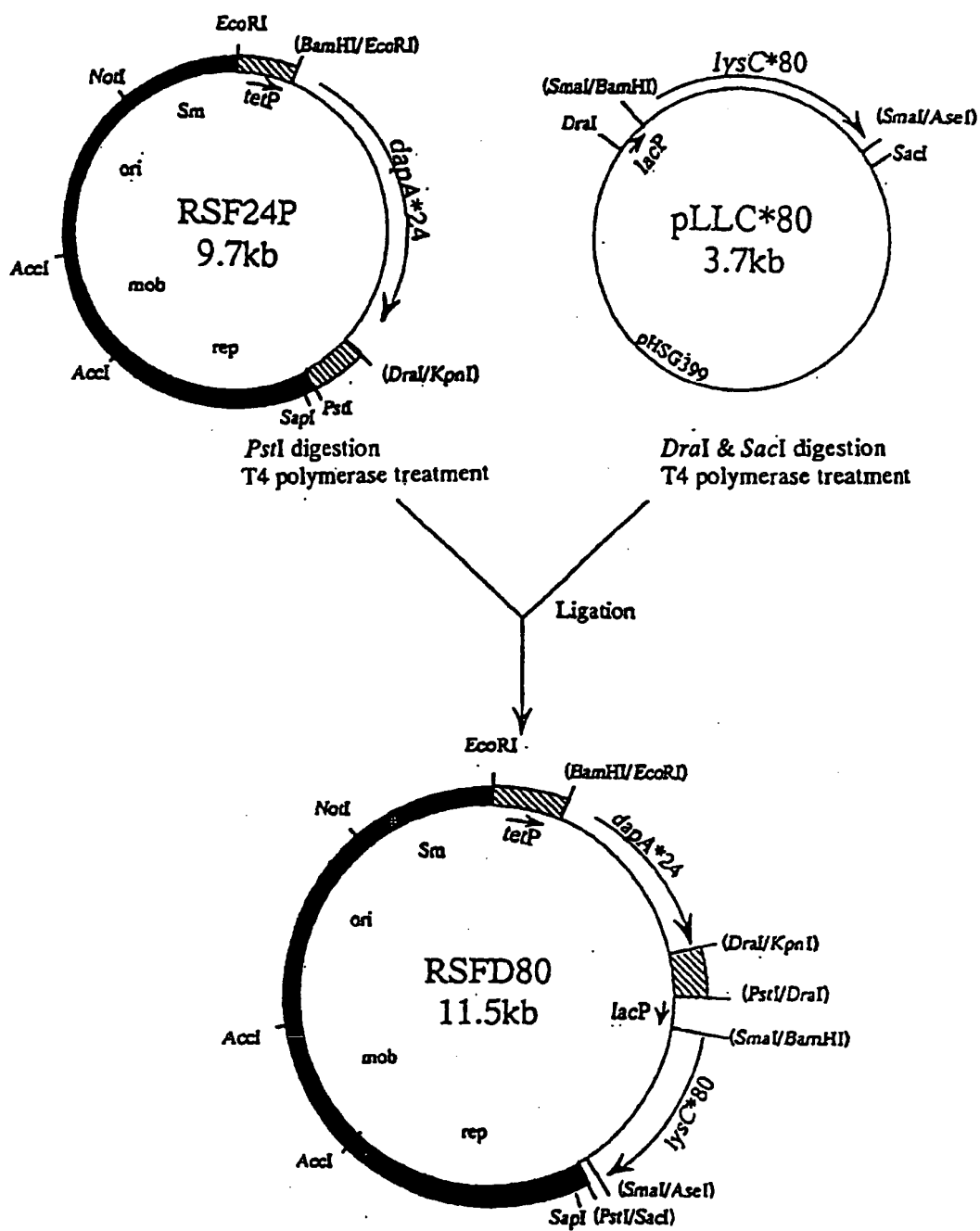


FIG. 2

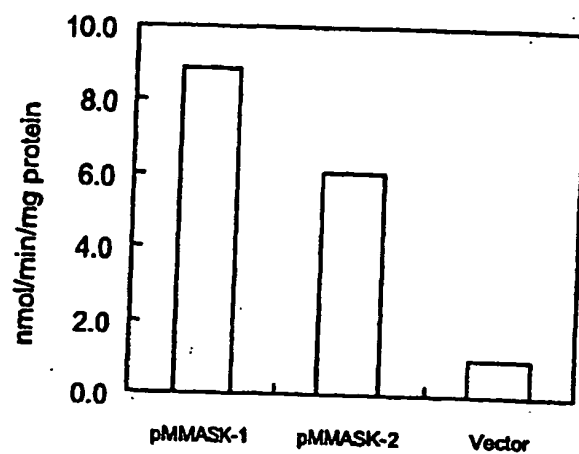


FIG. 3

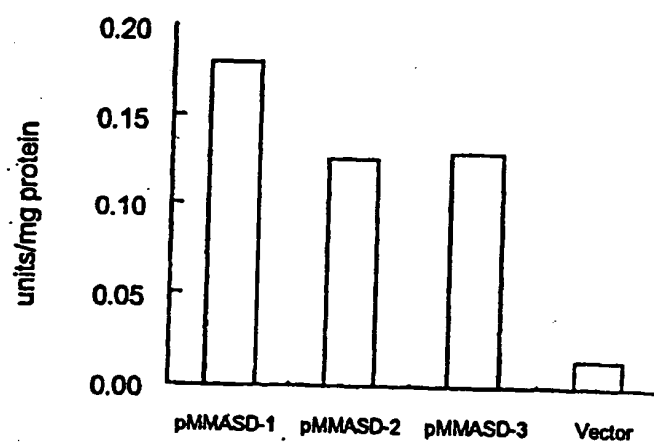


FIG. 4

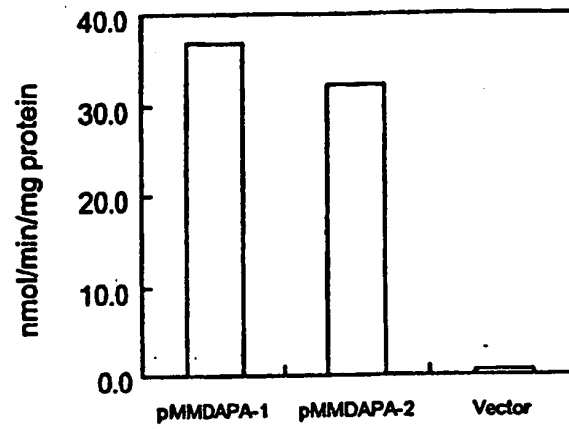


FIG. 5

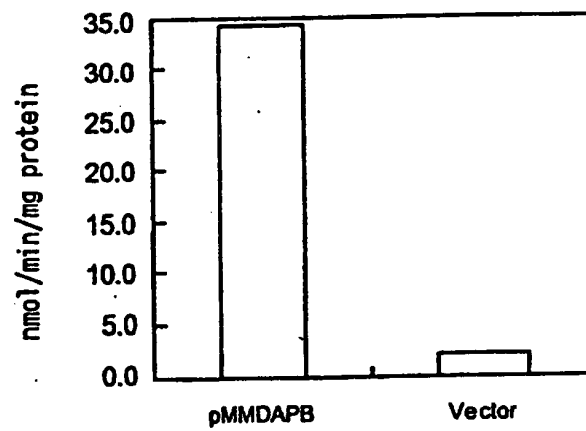


FIG. 6

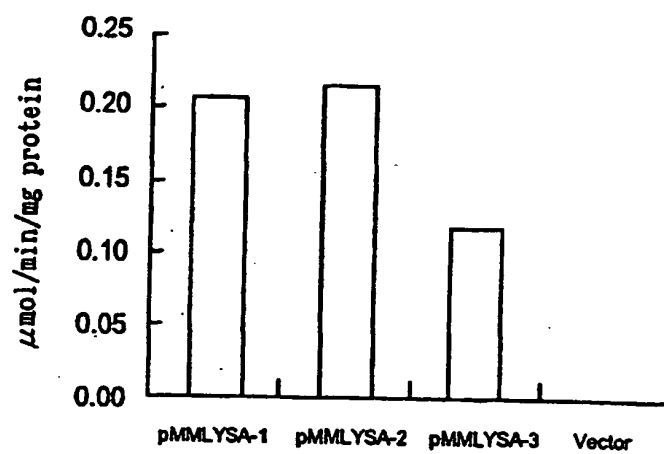


FIG. 7

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP00/02295

A. CLASSIFICATION OF SUBJECT MATTER Int.Cl ⁷ C12N1/21, 1/32, 9/00, 15/52, C12P13/04		
According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) Int.Cl ⁷ C12N1/20-1/21, 9/00-9/99, 15/52-15/61, C12P13/04-13/14		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched		
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) GenBank/EMBL/DBJ/GeneSeq, SwissProt/PIR/GeneSeq, WPI(DIALOG), BIOSIS(DIALOG)		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EP, 35831, A2 (IMPERIAL CHEMICAL INDUSTRIES LIMITED), 16 September, 1981 (16.09.81) & NO, 8100773, A & DK, 8100952, A & JP, 56-140893, A & PT, 72630, A & CA, 1187011, A & DE, 3173415, G & RO, 92662, A	1, 4, 11-14
X	WINDASS, J. D. et al., "Improved conversion of methanol to single-cell protein by Methylophilus methylotrophus", Nature, October 2, 1980, Volume 287, pp. 396-401	1, 4, 11-14
X	SCHENDEL, Frederick J. et al., "Cloning and Nucleotide Sequence of the Gene Coding for Aspartokinase II from a Thermophilic Methylophilic Bacillus sp.", Applied and Environmental Microbiology, September 1992, Volume 58, Number 9, pages 2806-2814 GenBank Accession No. M93419	17
X	HOANG, Tung T. et al., "Molecular genetic analysis of the region containing the essential Pseudomonas aeruginosa asd gene encoding aspartate- β -semialdehyde	19
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.		
* Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family		
Date of the actual completion of the international search 05 July, 2000 (05.07.00)		Date of mailing of the international search report 18 July, 2000 (18.07.00)
Name and mailing address of the ISA/ Japanese Patent Office		Authorized officer
Facsimile No.		Telephone No.

Form PCT/ISA/210 (second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP00/02295

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	dehydrogenase", Microbiology, March 1997, Volume 143, Part 3, pp. 899-907 GenBank Accession No. U11055	
X	YAMAMOTO, Yoshihiro et al., "Construction of a Contiguous 874-kb Sequence of the Escherichia coli-K12 Genome corresponding to 50.5-68.8 min on the Linkage Map and Analysis of Its Sequence Features", DNA Research, April 28, 1997, Volume 4, Number 2, pp.91-113 GenBank Accession No. D90877	21
X	BONNASSIE, S. et al., "Nucleotide sequence of the dapA gene from Corynebacterium glutamicum", Nucleic Acids Research, November 11, 1990, Volume 18, Number 21, page 6421 GenBank Accession No. X53993	21
X	BOUVIER, J. et al., "Nucleotide Sequence and Expression of the Escherichia coli dapB Gene", The Journal of Biological Chemistry, December 10, 1984, Volume 259, Number 23, pp.14829-14834 GenBank Accession No. M10611	23
X	DEKKERS, Linda C. et al., "A site-specific recombinase is required for competitive root colonization by Pseudomonas fluorescens WCS365", Proceedings of the National Academy of Sciences, USA, June 9, 1998, Volume 95, Number 12, pp.7051-7056 GenBank Accession No. Y12268	25
A	EP, 37273, A2 (IMPERIAL CHEMICAL INDUSTRIES LIMITED), 07 October, 1981 (07.10.81) & BR, 8101907, A & DK, 8101404, A & JP, 57-8782, A & ZA, 8102086, A & CA, 1187012, A & IL, 62514, A & DE, 3175828, G & KR, 8701127, B	1-25
A	WO, 96/41871, A1 (Ajinomoto Co., Inc.) 27 December, 1996 (27.12.96) & EP, 834559, A1 & SK, 9701705, A3 & CN, 1203629, A & HU, 9900149, A2 & US, 5989875, A & MX, 9710044, A1	1-25
A	Kerney, P. et al., "Regulation and routes of biosynthesis of serine and arginine in Methylophilus methylotrophus ASI", FEMS Microbiology Letters, July 1987, Volume 42, Nos.2-3, pp. 109- 112	1-25
A	JP, 1-235595, A (Kyowa Hakko Kogyo Co. Ltd.) 20 September, 1989 (20.09.89) (Family: none)	1-25
A	JP, 53-34987, A (Yoshiki Tani) 31 March, 1978 (31.03.78)	1-25

Form PCT/ISA/210 (continuation of second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP00/02295

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

The requirement of unity of invention in international application (PCT Rule 13.1) is not satisfied unless there is a technical relationship in a group of inventions involving one or more of the same or corresponding technical features. The term "technical feature" means a technical feature clearly showing the contribution to the prior art by the inventions as set forth in claims as a whole (PCT Rule 13.2). The requirement of unity of invention is judged without considering whether a group of inventions are described in separate claims or in a single claim in an alternative form (PCT Rule 13.3).

1. ☒ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest ☐ The additional search fees were accompanied by the applicant's protest.
☒ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP00/02295

Continuation of Box No. II of continuation of first sheet (1)

Inventions as set forth in claims 1 to 25 have a matter in common of a "bacterium belonging to the genus *Methylophilus* and having an L-amino acid productivity". However, document 1 (Japanese Patent Laid-Open No. 140893/1981) and document 2 (Nature, 287(5781), 396-401 (1980)) describe a bacterium belonging to the genus *Methylophilus* and carrying *Escherichia coli*-origin glutamate dehydrogenase (GDH) gene transferred in a state of allowing the expression thereof. Furthermore, a process for producing an amino acid by culturing this bacterium is stated in document 1 (see, for example, claim 19 and thereafter). As also stated in the description (p. 13) of the present international application, GDH gene is a gene imparting an L-glutamic acid productivity to a bacterium belonging to the genus *Methylophilus*. Therefore, it can be said that the bacterium belonging to the genus *Methylophilus* as described in document 1 or document 2 is a "bacterium belonging to the genus *Methylophilus* and having an L-glutamic acid productivity". Accordingly, there had been publicly known a bacterium belonging to the genus *Methylophilus* and having a productivity of L-glutamic acid, i.e., one of L-amino acids. Thus, the "bacterium belonging to the genus *Methylophilus* and having an L-amino acid productivity" which is the matter common to inventions as set forth in claims 1 to 25 cannot be regarded as a "special technical feature" as defined in PCT Rule 13.2.

Also, there had been publicly known a dihydrodipicolinate synthase gene (i.e., a gene capable of imparting an L-lysine productivity to a bacterium belonging to the genus *Methylophilus*) originating in a bacterium belonging to the genus *Corynebacterium* (see, for example, document 3 (Nucleic Acids Res., 18(21), 6421 (1990))). Accordingly, the "special technical feature" common to inventions as set forth in claims 16 to 25 is not an "enzyme gene being usable in enhancing the L-lysine productivity of a bacterium belonging to the genus *Methylophilus*" but an "enzyme gene originating in a bacterium belonging to the genus *Methylophilus* and being usable in enhancing the L-lysine productivity of a bacterium belonging to the genus *Methylophilus*". Thus, it may be said that there is no "special technical feature" as defined in PCT Rule 13.2 between the group of inventions as set forth in claims 1 to 15 relating to a bacterium belonging to the genus *Methylophilus* and having an L-lysine productivity and the group of inventions as set forth in claims 16 to 25.

Such being the case, the claims involve the following six groups of inventions:

- ① inventions relating to a bacterium belonging to the genus *Methylophilus* and having an L-lysine productivity as set forth in claims 1 to 15;
- ② inventions relating to a bacterium belonging to the genus *Methylophilus* and having an L-valine productivity as set forth in claims 1 to 15;
- ③ inventions relating to a bacterium belonging to the genus *Methylophilus* and having an L-leucine productivity as set forth in claims 1 to 15;
- ④ inventions relating to a bacterium belonging to the genus *Methylophilus* and having an L-isoleucine productivity as set forth in claims 1 to 15;
- ⑤ inventions relating to a bacterium belonging to the genus *Methylophilus* and having an L-threonine productivity as set forth in claims 1 to 15; and
- ⑥ inventions as set forth in claims 16 to 25.